Wild type hdm2 (17-125)

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:45:30 ; Search time 80.8 Seconds
(without alignments)
483.929 Million cell updates/sec

Title: US-10-822-254-2
Perfect score: 553
Sequence: 1 SQIPASEQETLVRPKPLLLK.....NLVVVNQQESSDSGTSVSEN 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	553	100.0	284	2	AAR75494	Aar75494 Human dou
2	553	100.0	284	2	AAR75397	Aar75397 Human dou
3	553	100.0	491	2	AAR42175	Aar42175 Human MDM
4	553	100.0	491	2	AAR76696	Aar76696 Human MDM
5	553	100.0	491	2	AAW07887	Aaw07887 Human MDM
6	553	100.0	491	2	AAW15463	Aaw15463 Human MDM
7	553	100.0	491	2	AAW13380	Aaw13380 Human MDM
8	553	100.0	491	2	AAW13600	Aaw13600 Murine do
9	553	100.0	491	2	AAW48241	Aaw48241 Human MDM
10	553	100.0	491	2	AAW57241	Aaw57241 Human MDM
11	553	100.0	491	2	AAW42879	Aaw42879 Amino aci
12	553	100.0	491	2	AAW42971	Aaw42971 Amino aci
13	553	100.0	491	2	AAW94304	Aaw94304 Human MDM
14	553	100.0	491	3	AAY96567	Aay96567 MDM2 onco
15	553	100.0	491	4	AAB48284	Aab48284 Human MDM
16	553	100.0	491	5	AAE22654	Aae22654 Human Rin
17	553	100.0	491	5	AAE22698	Aae22698 Human Rin
18	553	100.0	491	5	AAE25913	Aae25913 Human dou
19	553	100.0	491	5	AAO15376	Aao15376 Human Dm2
20	553	100.0	491	7	ADD21815	Add21815 Human mdm
21	553	100.0	491	7	ADE61562	Ade61562 Human Pro
22	553	100.0	491	8	ADL23893	Adl23893 Human E3
23	553	100.0	491	8	ADO52353	Ado52353 Human p53
24	553	100.0	491	8	ADP12593	Adp12593 Protein e
25	553	100.0	491	8	ADN71936	Adn71936 MDM2 prot
26	553	100.0	491	8	ADQ19417	Adq19417 Human sof
27	553	100.0	1171	4	AAU32421	Aau32421 Novel hum
28	536.5	97.0	216	3	AAB08846	Aab08846 A human M
29	527.5	95.4	522	7	ADJ95152	Adj95152 Novel NOV
30	527.5	95.4	522	7	ADJ95154	Adj95154 Novel NOV
31	493.5	89.2	489	2	AAR42176	Aar42176 Murine MD
32	493.5	89.2	489	2	AAR76697	Aar76697 Mouse MDM
33	493.5	89.2	489	2	AAW07888	Aaw07888 Murine MD
34	493.5	89.2	489	2	AAW15464	Aaw15464 Murine MD
35	493.5	89.2	489	2	AAW48242	Aaw48242 Mouse MDM
36	493.5	89.2	489	2	AAW57246	Aaw57246 Mouse MDM
37	493.5	89.2	489	2	AAW42997	Aaw42997 Amino aci
38	493.5	89.2	489	2	AAW42972	Aaw42972 Amino aci
39	493.5	89.2	489	2	AAW94305	Aaw94305 Mouse MDM
40	493.5	89.2	489	5	AAE25914	Aae25914 Mouse dou
41	493.5	89.2	489	5	ABB57099	Abb57099 Mouse isc
42	493.5	89.2	489	5	AAO15375	Aao15375 Mouse Dm2
43	493.5	89.2	489	7	ADD21816	Add21816 Mouse mdm
44	493.5	89.2	489	7	ADE61560	Ade61560 Rat Prote
45	352	63.7	227	2	AAR75495	Aar75495 Human dou

ALIGNMENTS

RESULT 1
AAR75494
ID AAR75494 standard; protein; 284 AA.
XX
AC AAR75494;
XX
DT 02-FEB-1996 (first entry)
XX
DE Human double minute 2 (hdm-2) antibody-binding region fragment 1.
XX
KW Human double minute gene 2; hdm-2; antibody binding region; antigen;
KW cancer; sarcoma; rhabdomyosarcoma; diagnosis; immunoassay.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1. .284
FT /note= "amino acids 1-284 of hdm-2 gene product"
XX
PN DE4339533-A1.
XX
PD 14-JUN-1995.
XX
PF 19-NOV-1993; 93DE-04339533.
XX
PR 19-NOV-1993; 93DE-04339533.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Zentgraf H, Klein R, Frey M, Martens R;
XX
DR WPI; 1995-216248/29.
DR N-PSDB; AAQ92515.
XX
PT Detection of human double minute gene 2 (hdm-2) antibodies - by
PT incubation with new hdm-2 or antibody-binding hdm-2 fragments; useful in
PT the detection of specific cancers.
XX
PS Claim 11; Fig 1; 12pp; German.
XX
CC Fragments contg. amino acids 1-284, 58-284 and 58-491 of the hdm-2 (human
CC double minute 2) gene product are claimed. The overlapping protein
CC fragments contain binding regions for hdm-2- specific antibodies and are
CC useful for identifying such antibodies in a claimed immunoassay method.
CC The presence of anti-hdm-2 antibodies is diagnostic of certain forms of
CC cancer, e.g. rhabdomyosarcoma
XX
SQ Sequence 284 AA;

```
  Query Match           100.0%;  Score 553;  DB 2;  Length 284;
  Best Local Similarity  100.0%;  Pred. No. 3.6e-64;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 2
AAR75397
ID   AAR75397 standard; protein; 284 AA.
XX
AC   AAR75397;
XX
DT   25-MAR-2003  (revised)
DT   25-JAN-1996  (first entry)
XX
DE   Human double minute 2 (hdm-2) antibody-binding region fragment 1.
XX
KW   Human double minute gene 2; hdm-2; antibody binding region; antigen;
KW   cancer; sarcoma; rhabdomyosarcoma; diagnosis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .284
FT                   /note= "amino acids 1-284 of hdm-2 gene product"
XX
PN   DE4345249-A1.
XX
PD   24-MAY-1995.
XX
PF   19-NOV-1993;   93DE-04345249.
XX
PR   19-NOV-1993;   93DE-04339533.
XX
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI   Zentgraf H,  Klein R,  Frey M,  Martens R;
XX
DR   WPI; 1995-195167/26.
DR   N-PSDB; AAQ87261.
XX
PT   New hdm-2 fragments contg. antibody binding region - used to detect
PT   specific antibodies for diagnosis of cancers, also new DNA sequences
PT   encoding them.
XX
PS   Claim 2; Fig 1; 11pp; German.
XX
CC   Fragments contg. amino acids 1-284, 58-284 and 58-491 of the hdm-2 (human
CC   double minute 2) gene product are claimed. The overlapping protein
CC   fragments contain binding regions for hdm-2- specific antibodies and are
CC   useful for identifying such antibodies. The presence of anti-hdm-2
CC   antibodies is diagnostic of certain forms of cancer, e.g.
CC   rhabdomyosarcoma. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 284 AA;

  Query Match           100.0%;  Score 553;  DB 2;  Length 284;
  Best Local Similarity  100.0%;  Pred. No. 3.6e-64;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 3
AAR42175
ID   AAR42175 standard; protein; 491 AA.
XX
AC   AAR42175;
XX
DT   25-MAR-2003  (revised)
DT   05-MAY-1994  (first entry)
XX
DE   Human MDM2.
XX
KW   p53 gene; tumour suppressor gene; regulation; cellular proliferation;
KW   cellular transformation; carcinoma; human; tumour; MDM2; inhibition;
KW   gene amplification.
XX
OS   Homo sapiens.
XX
PN   WO9320238-A2.
XX
PD   14-OCT-1993.
XX
PF   07-APR-1993;   93WO-US003199.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Burrell M,  Hill DE,  Kinzler KW,  Vogelstein B;
XX
DR   WPI; 1993-336944/42.
DR   N-PSDB; AAQ49891.
XX
PT   Diagnosing neoplasia from amplification of MDM2 gene - or elevated gene
PT   expression, also new DNA, MDM2 protein, antibodies and treatment of
PT   sarcoma by inhibiting MDM2 expression.
XX
PS   Claim 19; Fig 1; 75pp; English.
XX
CC   This sequence is encoded by the MDM2 gene. Amplification of the MDM2 gene
CC   is diagnostic of neoplasia or the potential for neoplasia. The protein
CC   encoded by this gene interacts with the product of the p53 gene. p53 is a
CC   tumour suppressor gene and encodes a protein which appears to be a member
CC   of a group of proteins which regulate normal cellular proliferation and
CC   suppression of cellular transformation. Inactivation of the p53 gene has
CC   been implicated in the formation, or progression of a wide variety of
CC   carcinoma. Polypeptides containing at least amino acids 13-41 of p53, or
CC   the DNA encoding these, may be used to inhibit the growth of tumour cells
CC   containing MDM2 gene amplification. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 491 AA;

  Query Match           100.0%;  Score 553;  DB 2;  Length 491;
  Best Local Similarity  100.0%;  Pred. No. 7.6e-64;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 4
AAR76696
ID   AAR76696 standard; protein; 491 AA.
```

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XX
AC   AAR76696;
XX
DT   16-OCT-2003  (revised)
DT   01-NOV-1995  (first entry)
XX
DE   Human MDM2 protein.
XX
KW   MDM2; sarcoma; diagnostic; DNA probe.
XX
OS   Homo sapiens; (cell line CaCo-2).
XX
PN   US5420263-A.
XX
PD   30-MAY-1995.
XX
PF   07-APR-1993;   93US-00044619.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Vogelstein B,  Kinzler KW;
XX
DR   WPI; 1995-206312/27.
DR   N-PSDB; AAQ94589.
XX
PT   New human MDM2 cDNA - used to develop prods. for use in the diagnosis and
PT   treatment of tumours.
XX
PS   Claim 1; Col 23-26; 34pp; English.
XX
CC   The human MDM2 gene is genetically altered (i.e. amplified) in human
CC   tumour cells. The human MDM2 protein binds to human p53 and allows the
CC   cell to escape from p53-regulated growth. Detecting that the gene has
CC   become amplified or detecting increased gene product expression (using
CC   probes, proteins, antibodies and inhibitors) allows diagnosis and therapy
CC   of cancers such as colorectal carcinoma, lung cancer and chronic
CC   myelogenous leukaemia. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ   Sequence 491 AA;

  Query Match             100.0%;  Score 553;  DB 2;  Length 491;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-64;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 5
AAW07887
ID   AAW07887 standard; protein; 491 AA.
XX
AC   AAW07887;
XX
DT   25-MAR-2003  (revised)
DT   28-JAN-1997  (first entry)
XX
DE   Human MDM-2, involved in tumour-development.
XX
KW   p53; MDM-2; binding-inhibitor; identification; tumour; cancer; neoplasia;
KW   antibody fusion protein; therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   166. .169
FT                   /label= phosphorylation_site
FT                   /note= "potential casein kinase II phosphorylation site"
FT   Binding-site    181. .185
FT                   /label= nuclear_localisation_signal
FT   Modified-site   192. .195
FT                   /label= phosphorylation_site
FT                   /note= "potential casein kinase II phosphorylation site"
FT   Domain          223. .274
FT                   /label= acid_activation_domain
FT   Modified-site   269. .272
FT                   /label= phosphorylation_site
FT                   /note= "potential casein kinase II phosphorylation site"
FT   Modified-site   290. .293
FT                   /label= phosphorylation_site
FT                   /note= "potential casein kinase II phosphorylation site"
FT   Domain          305. .322
FT                   /label= metal_binding_site
FT   Domain          461. .478
FT                   /label= metal_binding_site
XX
PN   US5550023-A.
XX
PD   27-AUG-1996.
XX
PF   18-MAY-1994;   94US-00245500.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
PR   07-APR-1993;   93US-00044619.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Vogelstein B,  Kinzler KW;
XX
DR   WPI; 1996-401591/40.
DR   N-PSDB; AAT45151.
XX
PT   Identification of cpds. interfering with human MDM2/p53 binding - useful
PT   as therapeutic agents to treat human neoplastic cells.
XX
PS   Claim 26; Col 25-28; 36pp; English.
XX
CC   AAW07887 represents human MDM-2 derived from a human colon carcinoma cell
CC   line, CaCo-2, cDNA library. The MDM-2 protein is used in a method for
CC   identifying compounds that interfere with the binding of p53 and MDM-2.
CC   In binding the p53 protein, the MDM-2 protein releases a cell from p53-
CC   regulated growth, allowing cancers to develop. Therefore compounds
CC   identified as interfering with the binding of MDM-2 to p53 are
CC   potentially useful in the treatment of human neoplastic cells. In the
CC   method pref. one or both of the proteins is a fusion protein esp. with an
CC   antibody or antibody fragment which aids separation and identification.
CC   (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 491 AA;

  Query Match             100.0%;  Score 553;  DB 2;  Length 491;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-64;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 6
AAW15463
ID   AAW15463 standard; protein; 491 AA.
XX
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AC   AAW15463;
XX
DT   25-MAR-2003  (revised)
DT   18-JUN-1997  (first entry)
XX
DE   Human MDM2.
XX
KW   Human; MDM2 protein; antibody; detection; cancer; diagnosis;
KW   p53-regulated growth.
XX
OS   Homo sapiens.
XX
PN   US5618921-A.
XX
PD   08-APR-1997.
XX
PF   17-FEB-1995;   95US-00390479.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
PR   07-APR-1993;   93US-00044619.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Vogelstein B,  Kinzler KW,  Burrell M,  Hill DE;
XX
DR   WPI; 1997-225474/20.
DR   N-PSDB; AAT66410.
XX
PT   Antibodies specific for human MDM2 protein - for diagnosis of cancer.
XX
PS   Claim 1; Col 19-24; 35pp; English.
XX
CC   This sequence represents the human MDM2 protein. Antibodies that
CC   specifically bind to human MDM2 protein may be used for detecting
CC   elevated expression of the MDM2 gene in a human tissue or body fluid
CC   sample, esp. for cancer diagnosis. The antibodies may be used to
CC   interfere with the binding of p53 to MDM2. Elevated levels of MDM2 appear
CC   to sequester p53 and allow the cell to escape from p53-regulated growth.
CC   (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 491 AA;

  Query Match             100.0%;  Score 553;  DB 2;  Length 491;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-64;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 7
AAW13380
ID   AAW13380 standard; protein; 491 AA.
XX
AC   AAW13380;
XX
DT   25-MAR-2003  (revised)
DT   05-JUN-1997  (first entry)
XX
DE   Human MDM2 protein.
XX
KW   Human; MDM2; CaCo-2; colonic; carcinoma; probe; detection; amplification;
KW   elevation; expression; diagnosis; neoplasia; neoplastic transformation;
KW   sarcoma; colorectal; lung cancer; chronic myelogenous leukaemia.
XX
OS   Homo sapiens.
XX
PN   US5606044-A.
XX
PD   25-FEB-1997.
XX
PF   17-FEB-1995;   95US-00390546.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
PR   07-APR-1993;   93US-00044619.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Kinzler KW,  Vogelstein B,  Hill DE,  Burrell M;
XX
DR   WPI; 1997-153623/14.
DR   N-PSDB; AAT62065.
XX
PT   Detection of amplification of human MDM2 gene - useful for diagnosis of
PT   neoplasia or potential neoplastic transformation.
XX
PS   Example 1; Col 21-24; 35pp; English.
XX
CC   The present sequence is the human MDM2 protein, the cDNA for which was
CC   isolated from a human CaCo-2 colonic carcinoma cell cDNA library using a
CC   murine MDM2 cDNA probe. The MDM2 cDNA can be used as a probe to detect
CC   the amplification or elevated expression of a human MDM2 gene, which is
CC   diagnostic of neoplasia or the potential for neoplastic transformation,
CC   useful for the detection of, e.g. sarcomas, colorectal carcinoma, lung
CC   cancer and chronic myelogenous leukaemia. (Updated on 25-MAR-2003 to
CC   correct PF field.)
XX
SQ   Sequence 491 AA;

  Query Match             100.0%;  Score 553;  DB 2;  Length 491;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-64;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 8
AAW13600
ID   AAW13600 standard; protein; 491 AA.
XX
AC   AAW13600;
XX
DT   16-JAN-1998  (first entry)
XX
DE   Murine double minute 2 protein sequence.
XX
KW   Mouse; Mdm2; murine double minute; phosphoprotein; binding; modulation;
KW   tumour suppressor; p53; oncogene; cell cycle arrest; p107; antagonist;
KW   inhibition; transcription factor; adenocarcinoma; colon; cancer; breast;
KW   lung; stomach; myeloid leukaemia; lymphoma; hyperproliferative;
KW   restenosis.
XX
OS   Mus musculus.
XX
PN   WO9709343-A2.
XX
PD   13-MAR-1997.
XX
PF   02-SEP-1996;   96WO-FR001340.
XX
PR   04-SEP-1995;   95FR-00010331.
XX
PA   (RHON ) RHONE POULENC RORER SA.
```

PA (INRM) INST NAT SANTE & RECH MEDICALE.
XX
PI Tocque B, Dubs-Poterszman M, Wasylyk B;
XX
DR WPI; 1997-192837/17.
DR N-PSDB; AAT61637.
XX
PT Treating cancer with antagonist of oncogenic activity of protein Mdm2 -
PT or nucleic acid encoding an antagonist, also viral vectors contg. this
PT nucleic acid.
XX
PS Claim 2; Page 26-30; 43pp; French.
XX
CC This is the amino acid sequence of the mouse Mdm2 (murine double minute-
CC 2) protein, a 90 kD phosphoprotein which binds and modulates the activity
CC of the tumour suppressor protein p53. It has now been shown that the mdm2
CC protein itself has oncogenic properties, especially in a p53-null
CC background. Mdm2 is observed to unblock cell cycle arrest in G1 caused by
CC over-expression of the p107 protein. This is especially done by the
CC region covering amino acid 1-134. The invention therefore relates to
CC antagonists able to inhibit the oncogenic activity of mdm2. These include
CC fragments of the p53 protein, especially amino acids 1-52, 1-41, 6-41, 16
CC -25 or 18-23 (AAW13602-6), or fragments of transcription factors e.g.
CC TFII, TBP or TAF250, which bind amino acids 1-134 of mdm2. Other
CC inhibitors include compounds which disrupt binding to region 135-491 of
CC mdm2, e.g. Rb, L5 or the transcription factor E2F. The antagonists are
CC used to treat e.g. adenocarcinoma of the colon; cancer of the breast,
CC lung or stomach; myeloid leukaemia; B cell lymphoma, or other
CC hyperproliferative conditions such as restenosis
XX
SQ Sequence 491 AA;

Query Match 100.0%; Score 553; DB 2; Length 491;
Best Local Similarity 100.0%; Pred. No. 7.6e-64;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
|||||||||||||||||||||||||||||||||||||||||||||||||||
Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125

RESULT 9
AAW48241
ID AAW48241 standard; protein; 491 AA.
XX
AC AAW48241;
XX
DT 18-JUN-1998 (first entry)
XX
DE Human MDM2.
XX
KW Human; MDM2; hMDM2; tumour; cancer; diagnosis; neoplastic disease;
KW sarcoma; liposarcoma; malignant fibrous histiocytoma; osteosarcoma.
XX
OS Homo sapiens.
XX
PN US5736338-A.
XX
PD 07-APR-1998.
XX
PF 17-FEB-1995; 95US-00390517.
XX
PR 07-APR-1992; 92US-00867840.
PR 23-JUN-1992; 92US-00903103.
PR 07-APR-1993; 93US-00044619.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Vogelstein B, Kinzler KW, Hill DE, Burrell M;
XX
DR WPI; 1998-239206/21.
DR N-PSDB; AAV20549.
XX
PT Cancer diagnosis - by determination of MDM2 protein.
XX
PS Claim 1; Col 25-28; 35pp; English.
XX
CC The present sequence represents human MDM2 (hMDM2) which is used in the
CC method of the present invention. The present invention describes a method
CC for diagnosing a neoplastic disease caused by overexpression of MDM2
CC protein. The method comprises detecting an elevated cellular amount of
CC this protein. The method is useful for the diagnosis of sarcoma,
CC especially liposarcoma, malignant fibrous histiocytoma or osteosarcoma
XX
SQ Sequence 491 AA;

Query Match 100.0%; Score 553; DB 2; Length 491;
Best Local Similarity 100.0%; Pred. No. 7.6e-64;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
|||||||||||||||||||||||||||||||||||||||||||||||||||
Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125

RESULT 10
AAW57241
ID AAW57241 standard; protein; 491 AA.
XX
AC AAW57241;
XX
DT 10-AUG-1998 (first entry)
XX
DE Human MDM2 protein.
XX
KW Human; p53; MDM2; tumour; growth inhibition; amplification;
KW malignant fibrous histiocytoma; liposarcoma.
XX
OS Homo sapiens.
XX
PN US5756455-A.
XX
PD 26-MAY-1998.
XX
PF 17-FEB-1995; 95US-00390515.
XX
PR 07-APR-1992; 92US-00867840.
PR 23-JUN-1992; 92US-00903103.
PR 07-APR-1993; 93US-00044619.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Vogelstein B, Kinzler KW;
XX
DR WPI; 1998-321574/28.
DR N-PSDB; AAV28876.
XX
PT Inhibiting growth of tumour cells having MDM2 gene amplification - with
PT p53 protein fragment.
XX
PS Claim 1; Col 23-28; 40pp; English.
XX
CC A method has been developed for inhibiting the growth of tumour cells
CC containing a human MDM2 gene amplification. The method comprises treating
CC the tumour cells with a DNA molecule that expresses a polypeptide capable
CC of binding to human MDM2 protein. The present sequence represents human
CC MDM2 protein. The present invention describes three preferred
CC polypeptides for binding human MDM2: (1) the polypeptide comprises amino

```
CC   acids 1-50 of p53 (see AAW57240); (2) the polypeptide comprises amino
CC   acids 13-41 of p53 (see AAW57240) and at least none additional p53
CC   residues on the N- or C-terminal side, provided that the polypeptide
CC   lacks the homooligomerisation domain of p53; (3) the polypeptide
CC   comprises amino acids 13-41 of p53 (see AAW57241) and at least nine
CC   additional p53 residues on the N- or C-terminal side, provided that the
CC   polypeptide lacks amino acids 138-393 of p53. Some malignant fibrous
CC   histiocytomas and liposarcomas have an MDM2 gene amplification, so
CC   detection of increased expression of MDM2 gene products indicates
CC   tumourigenesis
XX
SQ   Sequence 491 AA;

  Query Match             100.0%;  Score 553;  DB 2;  Length 491;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-64;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 11
AAW42879
ID   AAW42879 standard; protein; 491 AA.
XX
AC   AAW42879;
XX
DT   30-APR-1998  (first entry)
XX
DE   Amino acid sequence of human MDM2.
XX
KW   MDM2; tumour; diagnosis; neoplasia; DNA binding protein; p53 polypeptide;
KW   binding; tumour cell; p53-regulated growth; inhibition;
KW   anti-cancer agent.
XX
OS   Homo sapiens.
XX
PN   US5708136-A.
XX
PD   13-JAN-1998.
XX
PF   17-FEB-1995;   95US-00390516.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
PR   07-APR-1993;   93US-00044619.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Vogelstein B,  Kinzler KW,  Burrell M,  Hill DE;
XX
DR   WPI; 1998-100408/09.
XX
PT   Human MDM2 binding polypeptide - comprises fragments of p53, useful in re
PT   -establishing p53-regulated growth control in cells over-expressing MDM2.
XX
PS   Disclosure; Col 23-28; 41pp; English.
XX
CC   The present sequence represents human MDM2. The MDM2 gene is amplified in
CC   some human tumours. The amplification of this gene is diagnostic of
CC   neoplasia or its potential. It is speculated that the MDM2 protein is a
CC   potential DNA binding protein that functions in the modulation of
CC   expression of other genes and, when present in excess, inteferes with
CC   normal constraints on cell growth. A cell containing three recombinant
CC   DNA constructs was produced. These constructs encode an MDM2 protein
CC   fused to a sequence-specific DNA binding domain, a p53 polypeptide fused
CC   to a transcriptional activation domain, and a reporter gene downstream
CC   from a DNA element which is recognised by the sequence-specific DNA-
CC   binding domain. The cell is used to identify a compound which interferes
CC   with the binding of MDM2 and p53. Since MDM2 is overexpressed in tumour
CC   cells and since binding of MDM2 to p53 appears to allow tumour cells to
CC   escape from p53-regulated growth, compounds that inhibit such binding
CC   would be useful as anti-cancer agents
XX
SQ   Sequence 491 AA;

  Query Match             100.0%;  Score 553;  DB 2;  Length 491;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-64;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 12
AAW42971
ID   AAW42971 standard; protein; 491 AA.
XX
AC   AAW42971;
XX
DT   29-APR-1998  (first entry)
XX
DE   Amino acid sequence of human MDM2.
XX
KW   MDM2; tumour; diagnosis; neoplasia; DNA binding protein; p53 polypeptide;
KW   binding; tumour cell; p53-regulated growth; inhibition;
KW   anti-cancer agent.
XX
OS   Homo sapiens.
XX
PN   US5702903-A.
XX
PD   30-DEC-1997.
XX
PF   13-NOV-1995;   95US-00557393.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
PR   07-APR-1993;   93US-00044619.
PR   18-MAY-1994;   94US-00245500.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Vogelstein B,  Kinzler KW;
XX
DR   WPI; 1998-076411/07.
DR   N-PSDB; AAV03607.
XX
PT   Cell containing reporter construct containing human MDM2 and p53 genes -
PT   for identifying compounds that interfere with binding of human MDM2 to
PT   human p53, useful as anti-cancer agents.
XX
PS   Disclosure; Coulmns 22-28; 37pp; English.
XX
CC   The present sequence represents human MDM2. The MDM2 gene is amplified in
CC   some human tumours. The amplification of this gene is diagnostic of
CC   neoplasia or its potential. It is speculated that the MDM2 protein is a
CC   potential DNA binding protein that functions in the modulation of
CC   expression of other genes and, when present in excess, inteferes with
CC   normal constraints on cell growth. A cell containing three recombinant
CC   DNA constructs was produced. These constructs encode an MDM2 protein
CC   fused to a sequence-specific DNA binding domain, a p53 polypeptide fused
CC   to a transcriptional activation domain, and a reporter gene downstream
CC   from a DNA element which is recognised by the sequence-specific DNA-
CC   binding domain. The cell is used to identify a compound which interferes
CC   with the binding of MDM2 and p53. Since MDM2 is overexpressed in tumour
```

```
CC   cells and since binding of MDM2 to p53 appears to allow tumour cells to
CC   escape from p53-regulated growth, compounds that inhibit such binding
CC   would be useful as anti-cancer agents
XX
SQ   Sequence 491 AA;

  Query Match             100.0%;  Score 553;  DB 2;  Length 491;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-64;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 13
AAW94304
ID   AAW94304 standard; protein; 491 AA.
XX
AC   AAW94304;
XX
DT   13-APR-1999  (first entry)
XX
DE   Human MDM2.
XX
KW   Human; MDM2; p53; tumourigenesis; growth regulation; diagnosis;
KW   malignant fibrous histocytoma; MFH; liposarcoma.
XX
OS   Homo sapiens.
XX
PN   US5858976-A.
XX
PD   12-JAN-1999.
XX
PF   14-FEB-1997;   97US-00801718.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
PR   07-APR-1993;   93US-00044619.
PR   17-FEB-1995;   95US-00390515.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Kinzler KW,  Vogelstein B;
XX
DR   WPI; 1999-152105/13.
DR   N-PSDB; AAX03947.
XX
PT   Inhibiting growth of tumour cells having MDM2 gene amplification - with
PT   MDM2-binding p53 fragment.
XX
PS   Claim 1; Col 23-28; 41pp; English.
XX
CC   The present invention describes: (1) a method for inhibiting the growth
CC   of tumour cells which contain a human MDM2 gene amplification, comprising
CC   administering to the cells a DNA molecule that expresses a polypeptide
CC   consisting of a portion of p53 i.e. amino acids 13-41 of the 64 amino
CC   acid sequence given in AAW94303, the polypeptide being capable of binding
CC   to human MDM2 (the present sequence); (2) a method as in (1) where the
CC   polypeptide lacks the homo-oligomerisation domain of p53; and (3) a
CC   method as in (1) where the polypeptide lacks amino acids 138-393 of p53.
CC   The method is useful for treating the following tumour types which have a
CC   MDM2 gene amplification: M-7 malignant fibrous histocytoma (MFH), M-20
CC   MFH, L-9 liposarcoma, KL7 liposarcoma, KL28 liposarcoma, KL30
CC   liposarcoma, and OSA-CL MFH
XX
SQ   Sequence 491 AA;

  Query Match             100.0%;  Score 553;  DB 2;  Length 491;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-64;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 14
AAY96567
ID   AAY96567 standard; protein; 491 AA.
XX
AC   AAY96567;
XX
DT   12-SEP-2000  (first entry)
XX
DE   MDM2 oncoprotein.
XX
KW   hEST2; telomerase; catalytic subunit; reverse transcriptase; life-span;
KW   retinoblastoma; p53; tumour suppressor; inhibitor; arteriosclerosis;
KW   proliferation; immortal; tumour therapy; macular degeneration; activator;
KW   INK4; MDM2; oncoprotein.
XX
OS   Homo sapiens.
XX
PN   WO200031238-A2.
XX
PD   02-JUN-2000.
XX
PF   24-NOV-1999;   99WO-US027907.
XX
PR   25-NOV-1998;   98US-0109891P.
PR   17-FEB-1999;   99US-0120549P.
XX
PA   (GENE-) GENETICA INC.
XX
PI   Hannon GJ,  Beach DH;
XX
DR   WPI; 2000-400055/34.
DR   N-PSDB; AAA29389.
XX
PT   New method for increasing the proliferative capacity of cell lines
PT   comprises administering agents reversibly activating telomerase activity
PT   and reversibly inactivating Rb/INk4 and/or p53 pathways useful in
PT   treating age related diseases.
XX
PS   Claim 5; Page 120; 123pp; English.
XX
CC   The invention concerns methods and reagents for extending the life-span,
CC   e.g. the number of mitotic divisions, of a cell. The method relies on
CC   activation of a telomerase activity and inhibition of one or both of a
CC   retinoblastoma (Rb)/INK4 pathway or a p53 pathway. Phosphorylation of Rb
CC   by cyclin-dependent kinases, cdk4 and cdk6, releases the cells into the
CC   division cycle. Binding of INK4 family members, e.g. the tumour
CC   suppressor p16INK4a, inhibits kinase activity and results in growth
CC   arrest. Rb inactivators can selectively and reversibly inactivate an
CC   Rb/INK4 pathway, especially an Rb/p16INK4a pathway. The oncoprotein MDM2
CC   is a cellular inhibitor of Rb/E2F function and the p53 tumour suppressor
CC   and can also be used in the methods. Other molecules which can be used
CC   include cdk4 or cdk6 mutants. In particular, a cdk4 mutant is one which
CC   differs from at one or more of residues K22, R24, H95 and/or D97.
CC   Additional constructs include a papilloma virus E7 protein, or other
CC   viral oncoprotein which bypasses Rb and/or p53. Antisense constructs of
CC   the Rb and p16INK4a genes may also be used. The methods are useful for
CC   increasing the proliferative capacity of cells. The cells are
CC   subsequently of use in pharmaceutical and cosmetic preparations used to
CC   treat conditions related to (premature) ageing, e.g. macular degeneration
CC   and arteriosclerosis. The cells can also be used to replace tumour cell
CC   lines in vitro and for studies on biochemical and physiological aspects
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CC   of growth and differentiation. Long lived (immortal) cells could also be
CC   of use in the production of normal or genetically engineered
CC   biotechnology products
XX
SQ   Sequence 491 AA;

  Query Match             100.0%;  Score 553;  DB 3;  Length 491;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-64;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 15
AAB48284
ID   AAB48284 standard; protein; 491 AA.
XX
AC   AAB48284;
XX
DT   02-APR-2001  (first entry)
XX
DE   Human MDM2 protein.
XX
KW   S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF;
KW   CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;
KW   Bad; Bcl-2; tumour; cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO200075184-A1.
XX
PD   14-DEC-2000.
XX
PF   05-JUN-2000; 2000WO-US015449.
XX
PR   04-JUN-1999;   99US-0137494P.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Zhang H,  Tsvetkov LM,  Kondo T;
XX
DR   WPI; 2001-061703/07.
DR   N-PSDB; AAC84596.
XX
PT   Modulating polypeptide levels in a cell, diagnosing and treating tumor,
PT   involves altering levels of proteins such as S-phase kinase associated
PT   proteins 1, 2 and cullin/CDC53 proteins.
XX
PS   Claim 5; Page 93-95; 162pp; English.
XX
CC   The invention relates to methods of altering the polypeptide levels in a
CC   cell, using proteins selected from S-phase kinase associated proteins 1
CC   and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the
CC   cullin/ CDC53 family of proteins). The method is useful for altering the
CC   level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2
CC   polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for
CC   detecting tumours, and in monitoring tumor treatment in a mammal. Agents
CC   that modulate interactions between SKP and target proteins are useful for
CC   treating tumours
XX
SQ   Sequence 491 AA;

  Query Match             100.0%;  Score 553;  DB 4;  Length 491;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-64;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


Search completed: January 27, 2005, 18:06:15
Job time : 83.8 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:52:56 ; Search time 19.8 Seconds
(without alignments)
529.678 Million cell updates/sec

Title: US-10-822-254-2
Perfect score: 553
Sequence: 1 SQIPASEQETLVRPKPLLLK.....NLVVVNQQESSDSGTSVSEN 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	553	100.0	491	1	S24354	p53-binding protei
2	493.5	89.2	489	2	S15349	mdm2 protein - mou
3	276.5	50.0	489	2	S71955	MDM2-like p53-bind
4	78	14.1	685	1	SXBPT4	NAD+-protein ADP-r
5	78	14.1	698	1	S31630	NAD+-protein ADP-r
6	78	14.1	698	1	S31714	NAD+-protein ADP-r
7	76	13.7	967	2	A64710	type III restricti
8	72.5	13.1	565	2	S52682	hypothetical prote
9	72	13.0	969	2	E71810	type III restricti
10	71.5	12.9	514	2	D85069	hypothetical prote
11	70.5	12.7	422	2	T26334	hypothetical prote
12	70.5	12.7	838	2	I45557	eyeless, long form
13	69.5	12.6	339	2	A90395	conserved hypothet
14	69	12.5	181	2	S75415	probable ribosomal
15	68.5	12.4	277	2	AI0589	conserved hypothet
16	68.5	12.4	331	2	B84938	flagellar motor sw
17	68.5	12.4	517	2	S32169	hypothetical prote
18	68.5	12.4	709	2	E64213	DNA topoisomerase
19	68	12.3	860	2	S64366	hypothetical prote
20	68	12.3	3092	2	S46009	GTPase-activating
21	67.5	12.2	317	2	F97701	hypothetical prote
22	67.5	12.2	401	2	F90288	hypothetical prote
23	67.5	12.2	467	2	T25848	hypothetical prote
24	67	12.1	206	1	XUBYMC	methylated-DNA-[pr
25	67	12.1	261	2	H71680	exodeoxyribonuclea
26	66.5	12.0	447	2	I64002	sodium-translocati
27	66.5	12.0	826	2	B55363	desmocollin, type
28	66.5	12.0	891	2	S27029	preprotein translo
29	66.5	12.0	896	2	A55363	desmocollin, type
30	66.5	12.0	2833	2	A43360	inositol 1,4,5-tri
31	66	11.9	134	2	G69382	response regulator
32	66	11.9	322	2	G64388	hypothetical prote
33	65.5	11.8	455	2	S56695	1-aminocyclopropan
34	65.5	11.8	1268	2	T50252	probable transcrip
35	65	11.8	232	2	E82501	hypothetical prote
36	65	11.8	848	2	E86443	probable G-protein
37	64.5	11.7	245	2	F64347	hypothetical prote
38	64.5	11.7	485	1	S19677	1-aminocyclopropan
39	64.5	11.7	704	2	H82381	toxin secretion AT
40	64.5	11.7	1183	2	T39233	probable Inositol
41	64	11.6	260	2	T28182	hypothetical prote
42	64	11.6	286	2	B97743	exodeoxyribonuclea
43	64	11.6	292	2	S73692	probable GTPase/GT
44	64	11.6	346	2	G72094	ct244 hypothetical
45	64	11.6	346	2	G86528	CT244 hypothetical

ALIGNMENTS

RESULT 1
S24354
p53-binding protein mdm2 - human
N;Alternate names: mdm-2 oncogene; mouse double minute 2 homolog; p53-associated phospho
N;Contains: p53-binding protein mdm2, splice form A
C;Species: Homo sapiens (man)
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C;Accession: S24354; S57338; G02026
R;Oliner, J.D.; Kinzler, K.W.; Meltzer, P.S.; George, D.L.; Vogelstein, B.
Nature 358, 80-83, 1992
A;Title: Amplification of a gene encoding a p53-associated protein in human sarcomas.
A;Reference number: S24354; MUID:92310576; PMID:1614537
A;Accession: S24354
A;Molecule type: mRNA
A;Residues: 1-491 <OLI>
A;Cross-references: EMBL:Z12020; NID:g35211; PIDN:CAA78055.1; PID:g35212
R;Zauberman, A.; Flusberg, D.; Haupt, Y.; Barak, Y.; Oren, M.
Nucleic Acids Res. 23, 2584-2592, 1995
A;Title: A functional p53-responsive intronic promoter is contained within the human mdm
A;Reference number: S57338; MUID:95380270; PMID:7651818
A;Accession: S57338
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-16,'P',18-24 <ZAU>
A;Cross-references: EMBL:U28935; NID:g904033; PIDN:AAA82237.1; PID:g904034
R;Lunec, J.
submitted to the EMBL Data Library, August 1995
A;Description: Multiple alternate spliced mdm2 transcripts with loss of p53 binding doma
A;Reference number: G09070
A;Accession: G02026
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-27,223-491 <LUN>
A;Cross-references: EMBL:U33199; NID:g992676; PIDN:AAA75514.1; PID:g992677
A;Experimental source: splice form A
C;Genetics:
A;Gene: GDB:MDM2
A;Cross-references: GDB:250456; OMIM:164785
A;Map position: 12q14.3-12q15
C;Superfamily: human p53-binding protein mdm2
C;Keywords: alternative splicing; oncogene; phosphoprotein
F;1-491/Product: p53-binding protein mdm-2 #status predicted <MAT1>
F;1-27,223-491/Product: p53-binding protein mdm-2, splice form A #status predicted <MAT2

Query Match 100.0%; Score 553; DB 1; Length 491;
Best Local Similarity 100.0%; Pred. No. 2.6e-49;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76
```

```
Qy          61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 2
S15349
mdm2 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S15349
R;Fakharzadeh, S.S.; Trusko, S.P.; George, D.L.
EMBO J. 10, 1565-1569, 1991
A;Title: Tumorigenic potential associated with enhanced expression of a gene that is amp
A;Reference number: S15349; MUID:91224107; PMID:2026149
A;Accession: S15349
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-489 <FAK>
A;Cross-references: UNIPROT:P23804; EMBL:X58876; NID:g53038; PIDN:CAA41684.1; PID:g53039
C;Genetics:
A;Gene: mdm2
C;Superfamily: human p53-binding protein mdm2

  Query Match             89.2%;  Score 493.5;  DB 2;  Length 489;
  Best Local Similarity   88.1%;  Pred. No. 3.6e-43;
  Matches   96;  Conservative    7;  Mismatches    3;  Indels    3;  Gaps    1;

Qy           1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
               |||||||||||||||||||||||||| ||||||::||:||||||||||||||||||||
Db          17 SQIPASEQETLVRPKPLLLKLLKSVGAQNDTYTMKEIIFYIGQYIMTKRLYDEKQQHIVY 76

Qy          61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
               ||||||||:|||||||||||||| |||||| |:||   |||||:||:
Db          77 CSNDLLGDVFGVPSFSVKEHRKIYAMIYRNLVAVSQQ---DSGTSLSES 122


RESULT 3
S71955
MDM2-like p53-binding protein MDMX - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
C;Accession: S71955
R;Shvarts, A.; Steegenga, W.T.; Riteco, N.; van Laar, T.; Dekker, P.; Bazuine, M.; van H
EMBO J. 15, 5349-5357, 1996
A;Title: MDMX: a novel p53-binding protein with some functional properties of MDM2.
A;Reference number: S71955; MUID:97050840; PMID:8895579
A;Accession: S71955
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-489 <SHV>
A;Cross-references: UNIPROT:O35618; EMBL:AF007110; NID:g2253388; PIDN:AAB62927.1; PID:g2
C;Genetics:
A;Gene: MDMX
C;Function:
A;Description: inhibits transcription activation function of tumour suppressor protein p
C;Superfamily: human p53-binding protein mdm2

  Query Match             50.0%;  Score 276.5;  DB 2;  Length 489;
  Best Local Similarity   53.3%;  Pred. No. 9.2e-21;
  Matches   56;  Conservative   16;  Mismatches   22;  Indels   11;  Gaps    1;

Qy           5 ASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVYCSND 64
               :||| : |||| |||:| : ||| : :|||||: ||||||| |:|||:::||:|||  |
Db          20 SSEQISQVRPKLQLLKILHAAGAQGEVFTMKEVMHYLGQYIMVKQLYDQQEQHMVYCGGD 79

Qy          65 LLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
               ||||| |  |||||:   :| |: :|||           || | |
Db          80 LLGDLLGCQSFSVKDPSPLYDMLRKNLV----------TSASNN 113


RESULT 4
SXBPT4
NAD+-protein ADP-ribosyltransferase (EC 2.4.2.-) precursor - phage T4
C;Species: phage T4
A;Note: host Escherichia coli
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C;Accession: JU0096
R;Hilse, D.; Koch, T.; Rueger, W.
Nucleic Acids Res. 17, 6731, 1989
A;Title: Nucleotide sequence of the alt gene of bacteriophage T4.
A;Reference number: JU0096; MUID:89386005; PMID:2506526
A;Accession: JU0096
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-685 <HIL>
A;Cross-references: UNIPROT:P12726
C;Comment: This enzyme catalyzes the ADP-ribosylation of one of the two alpha-subunits o
C;Genetics:
A;Gene: alt
C;Superfamily: phage T4 NAD-protein ADP-ribosyltransferase
C;Keywords: glycosyltransferase; pentosyltransferase
F;7-685/Product: NAD-protein ADP-ribosyltransferase #status predicted <MAT>

  Query Match             14.1%;  Score 78;  DB 1;  Length 685;
  Best Local Similarity   28.0%;  Pred. No. 4.3;
  Matches   28;  Conservative   23;  Mismatches   35;  Indels   14;  Gaps    6;

Qy          18 LLKLLKS--VGAQKDTYTMKEVLFYL---GQYIMTKRL--YDEKQQHI-VYCSNDLLGDL 69
               :|::|||   |  :    : : |      |:|:: | |  ||:|  :| ::  |  | |:
Db         111 MLRILKSKTAGQARQIQVIADRLIRSRSGGRYVLLKELWDYDKKYAYILIHRKNVSLEDI 170

Qy          70 FGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
               |||  | :   |: : :    | :|:    |:|  |::|
Db         171 PGVPEISTELFTKVESKV--GDVYINK----DTGAQVTKN 204


RESULT 5
S31630
NAD+-protein ADP-ribosyltransferase (EC 2.4.2.-) precursor - phage T2
C;Species: phage T2
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S31630
R;Koch, T.; Rueger, W.
submitted to the EMBL Data Library, December 1992
A;Description: The ADP-ribosyltransferase of bacteriophages T2, T4 and T6: Sequencing of
A;Reference number: S31630
A;Accession: S31630
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-698 <KOC>
A;Cross-references: UNIPROT:Q38424; EMBL:X69893; NID:g15187; PIDN:CAA49517.1; PID:g15188
C;Superfamily: phage T4 NAD-protein ADP-ribosyltransferase
C;Keywords: glycosyltransferase; NAD; pentosyltransferase

  Query Match             14.1%;  Score 78;  DB 1;  Length 698;
  Best Local Similarity   28.0%;  Pred. No. 4.3;
  Matches   28;  Conservative   23;  Mismatches   35;  Indels   14;  Gaps    6;

Qy          18 LLKLLKS--VGAQKDTYTMKEVLFYL---GQYIMTKRL--YDEKQQHI-VYCSNDLLGDL 69
               :|::|||   |  :    : : |      |:|:: | |  ||:|  :| ::  |  | |:
Db         112 MLRILKSKTAGQARQIQVIADRLIRSRSGGRYVLLKELWDYDKKYAYILIHRKNVSLEDI 171

Qy          70 FGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
               |||  | :   |: : :    | :|:    |:|  |::|
Db         172 PGVPEISTELFTKVESKV--GDVYINK----DTGAQVTKN 205


RESULT 6
S31714
NAD+-protein ADP-ribosyltransferase (EC 2.4.2.-) precursor - phage T6
C;Species: phage T6
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S31714
R;Koch, T.; Rueger, W.
submitted to the EMBL Data Library, December 1992
```

```
A;Description: The ADP-ribosyltransferase of bacteriophages T2, T4 and T6: Sequencing of
A;Reference number: S31630
A;Accession: S31714
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-698 <KOC>
A;Cross-references: UNIPROT:Q38433; EMBL:X69894; NID:g15422; PIDN:CAA49518.1; PID:g15423
C;Superfamily: phage T4 NAD-protein ADP-ribosyltransferase
C;Keywords: glycosyltransferase; NAD; pentosyltransferase

  Query Match             14.1%;  Score 78;  DB 1;  Length 698;
  Best Local Similarity   28.0%;  Pred. No. 4.3;
  Matches   28;  Conservative   23;  Mismatches   35;  Indels   14;  Gaps    6;

Qy         18 LLKLLKS--VGAQKDTYTMKEVLFYL---GQYIMTKRL--YDEKQQHI-VYCSNDLLGDL 69
                :|::|||    |  :    : : |       |:|:: | |  ||:|  :| ::  |  | |:
Db        112 MLRILKSKTAGQARQIQVIADRLIRSRSGGRYVLLKELWDYDKKYAYILIHRKNVSLEDI 171

Qy         70 FGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
                |||  | :   |: : :    | :|:    |:|  |::|
Db        172 PGVPEISTELFTKVESKV--GDVYINK----DTGAQVTKN 205


RESULT 7
A64710
type III restriction enzyme R protein - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: A64710
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: A64710
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-967 <TOM>
A;Cross-references: UNIPROT:O26050; GB:AE000650; GB:AE000511; NID:g2314700; PIDN:AAD0856
C;Genetics:
A;Start codon: GTG

  Query Match             13.7%;  Score 76;  DB 2;  Length 967;
  Best Local Similarity   24.8%;  Pred. No. 10;
  Matches   26;  Conservative   22;  Mismatches   43;  Indels   14;  Gaps    3;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKR---LYDEKQQH 57
              ::|  :||| | | : | |:::      | :| |:|        |  ::    |||| :
Db        768 NEIKKNEQEGLRRLEELFLEIIYQNIKDKISYQMRETT------IKNRKNDAFYDEKGEI 821

Qy         58 IVYCSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDS 102
                :    |  | : : : ||:|       :| | : |: :   |:
Db        822 REFLDGSLGADKYEIKNSSVRE-----KCLYENFMQVDSEIEKDT 861


RESULT 8
S52682
hypothetical protein YDR117c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YD9727.12c
C;Species: Saccharomyces cerevisiae
C;Date: 19-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S52682
R;Murphy, L.; Shore, L.; Harris, D.
submitted to the EMBL Data Library, March 1995
A;Reference number: S52671
A;Accession: S52682
A;Molecule type: DNA
A;Residues: 1-565 <MUR>
A;Cross-references: UNIPROT:Q04600; EMBL:Z48758; NID:g747879; PID:g747891; GSPDB:GN00004
C;Genetics:
A;Gene: MIPS:YDR117c
A;Cross-references: SGD:S0002524
A;Map position: 4R

  Query Match             13.1%;  Score 72.5;  DB 2;  Length 565;
  Best Local Similarity   33.3%;  Pred. No. 13;
  Matches   25;  Conservative   11;  Mismatches   30;  Indels    9;  Gaps    3;

Qy         10 TLVRPKPLLLKLLKSVGAQKDT-YTMKEVLFYLGQYIMTKRLYDEKQQHIVYCSNDLLGD 68
              || :|  |   ||| |     | || :::   : |||  | | | | :  |   :||| |
Db        362 TLYKPFNLAKDLLKEVNLASHTYYTSQDIRSAVSQYISVKNLADTKDKGKV-IMDDLLFD 420

Qy         69 LFGVPSFSVKEHRKI 83
              :       | : :|:
Db        421 M-------VNKKKKV 428


RESULT 9
E71810
type III restriction enzyme - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: E71810
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: E71810
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-969 <ARN>
A;Cross-references: UNIPROT:Q9ZJA3; GB:AE001563; GB:AE001439; NID:g4156027; PIDN:AAD0698
A;Experimental source: strain J99
C;Genetics:
A;Gene: res_2

  Query Match             13.0%;  Score 72;  DB 2;  Length 969;
  Best Local Similarity   23.8%;  Pred. No. 26;
  Matches   25;  Conservative   22;  Mismatches   44;  Indels   14;  Gaps    3;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKR---LYDEKQQH 57
              ::|  :||| | | : | |:::      | :| |:|        |  ::    |||| :
Db        770 NEIKKNEQEGLKRLEELFLEIIYQNIKDKISYQMRETT------IKNRKNDAFYDEKGEI 823

Qy         58 IVYCSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDS 102
                :    |  | : : : | :|       :| | : |: :   |:
Db        824 REFLDGSLGADKYEIKNSSAQE-----KCLYENFMQVDSEIEKDT 863


RESULT 10
D85069
hypothetical protein AT4g05520 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: D85069
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: D85069
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-514 <STO>
A;Cross-references: UNIPROT:Q9S9W1; GB:NC_001268; NID:g7267312; PIDN:CAB81094.1; GSPDB:G
C;Genetics:
A;Gene: AT4g05520
A;Map position: 4

  Query Match             12.9%;  Score 71.5;  DB 2;  Length 514;
  Best Local Similarity   29.7%;  Pred. No. 14;
  Matches   27;  Conservative   13;  Mismatches   26;  Indels   25;  Gaps    4;
```

```
Qy          15 KPLLLKLLKSVGA-----QKDTYTMKEVLFYLGQY-----------IMTKRLYDEKQQHI 58
               :|| |||::  ||       |    | : |  |:| :            : | |::::|
Db         384 QPLFLKLMRVYGALMWSLGKVLNTPEVVRVYIGSFNDKPINEVAVGPIGKELFEKEQ--- 440

Qy          59 VYCSNDLLGDLFGVPSFSVKEHRKIYTMIYR 89
                 |||| ||  ||  :    |||   : |
Db         441 ----NDLLADLMDVPKKAC--DRKINEFVKR 465


RESULT 11
T26334
hypothetical protein W10G6.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Aug-2004
C;Accession: T26334
R;McMurray, A.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z20201
A;Accession: T26334
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-422 <WIL>
A;Cross-references: UNIPROT:Q94365; EMBL:Z81140; PIDN:CAB03485.1; GSPDB:GN00028; CESP:W1
A;Experimental source: clone W10G6
C;Genetics:
A;Gene: CESP:W10G6.2
A;Map position: X
A;Introns: 14/3; 60/2; 88/2; 135/3; 179/3; 217/2; 290/3; 393/1
C;Superfamily: protein kinase homology

  Query Match             12.7%;  Score 70.5;  DB 2;  Length 422;
  Best Local Similarity   27.6%;  Pred. No. 15;
  Matches   27;  Conservative   16;  Mismatches   34;  Indels   21;  Gaps    5;

Qy          12 VRPKPLLLK-----LLKSVG-------AQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIV 59
               ::|: |||      :|   |          | | |       ||   |: |: ||:
Db         219 LKPENLLLDDKGYLVLTDFGLCKEDMQGSKTTSTFCGTPEYLAPEIILKKPYDKTVDW-- 276

Qy          60 YCSNDLLGD-LFGVPSFSVKEHRKIYTMIYRNLVVVNQ 96
               :|   :| : :||:| |  |:| ::|  |      :||
Db         277 WCLGSVLYEMIFGLPPFYSKDHNEMYDKI------INQ 308


RESULT 12
I45557
eyeless, long form - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 16-Aug-2004
C;Accession: I45557
R;Quiring, R.; Walldorf, U.; Kloter, U.; Gehring, W.J.
Science 265, 785-789, 1994
A;Title: Homology of the eyeless gene of Drosophila to the Small eye gene in mice and An
A;Reference number: A54584; MUID:94323757; PMID:7914031
A;Accession: I45557
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-838 <RES>
A;Cross-references: EMBL:X79493; NID:g641809; PIDN:CAA56038.1; PID:g641810
C;Genetics:
A;Gene: FlyBase:ey
A;Cross-references: FlyBase:FBgn0005558
A;Introns: 37/1; 92/2; 152/3; 371/1; 429/1; 521/1; 639/2
C;Superfamily: homeobox homology; paired box homology
C;Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulati
F;37-161/Domain: paired box homology <PBH>
F;412-468/Domain: homeobox homology <HOX>

  Query Match             12.7%;  Score 70.5;  DB 2;  Length 838;
  Best Local Similarity   26.0%;  Pred. No. 32;
  Matches   26;  Conservative   14;  Mismatches   33;  Indels   27;  Gaps    5;

Qy          12 VRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQY------IMTKRLYDEKQQHIVYCSNDL 65
               :||        :::|  |      ||:  : ||      |    : |   |  | |:||

Db          99 IRP--------RAIGGSKPRVATAEVVSKISQYKRECPSIFAWEIRDRLLQENV-CTND- 148

Qy          66 LGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTS 105
                  :|| |           : |||    :|:|: ||:|
Db         149 -----NIPSVS------SINRVLRNLAAQKEQQSTGSGSS 177


RESULT 13
A90395
conserved hypothetical protein [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: A90395
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: A90395
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-339 <KUR>
A;Cross-references: UNIPROT:Q97WH1; GB:AE006641; NID:g13815550; PIDN:AAK42416.1; GSPDB:G
C;Genetics:
A;Gene: SSO2248

  Query Match             12.6%;  Score 69.5;  DB 2;  Length 339;
  Best Local Similarity   28.2%;  Pred. No. 14;
  Matches   24;  Conservative   20;  Mismatches   28;  Indels   13;  Gaps    5;

Qy          19 LKLLKSVGAQ-----KDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVYCSNDLLG-DLFGV 72
               |||:::|         ||   |:::|  | |::::| : :|   :::: |    | ||||
Db         154 LKLIRNVDLNGIISIKDERKMRDLLMLLNQFLVSK-IIEEYDGNVLWISKVSRGRDLFGT 212

Qy          73 --PSFSV----KEHRKIYTMIYRNL 91
                 |  :|     | |    :| :|:
Db         213 DYPDITVLELFTEKRGFSKLIIKNI 237


RESULT 14
S75415
probable ribosomal protein S4 - Sulfolobus solfataricus
N;Alternate names: protein c04049
C;Species: Sulfolobus solfataricus
C;Date: 11-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C;Accession: S75415
R;Sensen, C.W.; Klenk, H.P.; Singh, R.K.; Allard, G.; Chan, C.C.Y.; Liu, Q.Y.; Penny, S.
Mol. Microbiol. 22, 175-191, 1996
A;Title: Organizational characteristics and information content of an archaeal genome: 1
A;Reference number: S73076; MUID:97055432; PMID:8899719
A;Accession: S75415
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-181 <SEN>
A;Cross-references: UNIPROT:P95987; EMBL:Y08257; NID:g1707772; PIDN:CAA69529.1; PID:g170
A;Experimental source: strain P2
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1996
C;Superfamily: rat ribosomal protein S9
C;Keywords: protein biosynthesis; ribosome

  Query Match             12.5%;  Score 69;  DB 2;  Length 181;
  Best Local Similarity   24.2%;  Pred. No. 7.9;
  Matches   29;  Conservative   20;  Mismatches   39;  Indels   32;  Gaps    4;

Qy           9 ETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRL----YDEKQQHIVYCSND 64
               |  || | |: |||| :|:| |: ::|   | :: :||   | :  : :| :
Db          65 ERAVREKQLVGKLLKMGLLKKETATVDDILSLTEQDLLERRLQTIVYKKGLSNTIYQARQ 124

Qy          65 LL--------GDLFGVPSFSVKEHRKIYTMIYRNLV-------------VVNQQESSDSG 103
               |:       |  | : |    :      ||:             |::|||  : |
Db         125 LITHGHIAVNGKRVTSPGYIVNVDEE-------NLIDYYVTSSFKSRPPVMSQQEGGEIG 177
```

RESULT 15
AI0589
conserved hypothetical protein STY0767 [imported] - Salmonella enterica subsp. enterica
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AI0589
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AI0589
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-277 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD05187.1; PID:g16501958; GSPDB:GN00176
C;Genetics:
A;Gene: STY0767

  Query Match 12.4%; Score 68.5; DB 2; Length 277;
  Best Local Similarity 26.0%; Pred. No. 15;
  Matches 25; Conservative 16; Mismatches 28; Indels 27; Gaps 4;

```
Qy         11 LVRPKP----LLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVYCSNDLL 66
              :|| ||    ||:: |:|:  |    | |::                |::|  : |
Db          8 IVRHKPGRTRLLMRALQSINDQ----TFKKI----------------NIIIFCMEEEL 45

Qy         67 GDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDS 102
                 |  | :||   ||::||    : |  : |:|
Db         46 -KCHNVDDFYLKELSNIYSVIYDENCIFNAIKMSES 80
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Search completed: January 27, 2005, 18:15:08
Job time : 21.8 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:51:46 ; Search time 84.6 Seconds
(without alignments)
741.322 Million cell updates/sec

Title: US-10-822-254-2
Perfect score: 553
Sequence: 1 SQIPASEQETLVRPKPLLLK.....NLVVVNQQESSDSGTSVSEN 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	553	100.0	166	2	Q8NDW2	Q8ndw2 homo sapien
2	553	100.0	195	2	Q96DS4	Q96ds4 homo sapien
3	553	100.0	243	2	Q8TE47	Q8te47 homo sapien
4	553	100.0	491	1	MDM2_HUMAN	Q00987 homo sapien
5	553	100.0	491	2	AAP35922	Aap35922 homo sapi
6	553	100.0	491	2	AAH67077	Aah67077 homo sapi
7	541	97.8	487	1	MDM2_CANFA	P56950 canis famil
8	541	97.8	487	2	Q9GMZ6	Q9gmz6 canis famil
9	541	97.8	491	1	MDM2_HORSE	P56951 equus cabal
10	538	97.3	491	2	Q7YRZ8	Q7yrz8 felis silve
11	503	91.0	436	2	Q8WYJ2	Q8wyj2 homo sapien
12	493.5	89.2	489	1	MDM2_MOUSE	P23804 mus musculu
13	493.5	89.2	489	2	Q91XK7	Q91xk7 m mus muscu
14	476	86.1	118	2	Q8WYJ3	Q8wyj3 homo sapien
15	469.5	84.9	466	1	MDM2_MESAU	Q60524 mesocricetu
16	415	75.0	325	2	Q9PVL2	Q9pvl2 gallus gall
17	407	73.6	173	2	Q8TE46	Q8te46 homo sapien
18	358	64.7	473	1	MDM2_XENLA	P56273 xenopus lae
19	358	64.7	473	2	Q6GMB5	Q6gmb5 xenopus lae
20	357	64.6	482	2	Q6P3Q9	Q6p3q9 xenopus tro
21	357	64.6	482	2	AAH63898	Aah63898 xenopus t
22	339	61.3	105	2	Q8NDW0	Q8ndw0 homo sapien
23	320	57.9	426	2	Q9GK41	Q9gk41 canis famil
24	292.5	52.9	445	1	MDM2_BRARE	O42354 brachydanio
25	292.5	52.9	445	2	AAM00198	Aam00198 brachydan
26	280.5	50.7	446	2	Q8WYJ1	Q8wyj1 homo sapien
27	276.5	50.0	489	1	MDM4_MOUSE	O35618 mus musculu
28	273.5	49.5	489	2	Q9CYG1	Q9cyg1 m mus muscu
29	268	48.5	491	2	Q7ZUW7	Q7zuw7 brachydanio
30	267	48.3	490	2	Q99L86	Q99l86 mus musculu
31	266	48.1	475	2	Q7ZYI3	Q7zyi3 xenopus lae
32	254.5	46.0	134	2	Q6PHL8	Q6phl8 xenopus lae
33	254.5	46.0	134	2	AAH56503	Aah56503 xenopus l
34	251	45.4	153	2	Q6MZR7	Q6mzr7 homo sapien
35	251	45.4	153	2	CAE45961	Cae45961 homo sapi
36	251	45.4	490	2	AAH67299	Aah67299 homo sapi
37	249	45.0	490	1	MDM4_HUMAN	O15151 homo sapien
38	223	40.3	69	2	Q86WA4	Q86wa4 homo sapien
39	216	39.1	66	2	Q96DS3	Q96ds3 homo sapien
40	213	38.5	70	2	Q86WA3	Q86wa3 homo sapien
41	199	36.0	95	2	Q96DS1	Q96ds1 homo sapien
42	179.5	32.5	70	2	Q8NDW1	Q8ndw1 homo sapien
43	177	32.0	159	2	Q96DS0	Q96ds0 homo sapien
44	176	31.8	60	2	Q96DS5	Q96ds5 homo sapien
45	176	31.8	130	2	Q9H4C3	Q9h4c3 homo sapien

ALIGNMENTS

RESULT 1
Q8NDW2
ID Q8NDW2 PRELIMINARY; PRT; 166 AA.
AC Q8NDW2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE P53-binding protein.
GN Name=MDM2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bartel F., Pinkert D., Kappler M., Bache M., Schmidt H., Taubert H.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ491698; CAD36959.1; -.
DR HSSP; Q9UMT8; 1YCR.
DR GO; GO:0005634; C:nucleus; IEA.
DR InterPro; IPR010984; MDM2.
DR InterPro; IPR003121; SWIB_MDM2.
DR Pfam; PF02201; SWIB; 1.
SQ SEQUENCE 166 AA; 18900 MW; FA6B5BA18E85040D CRC64;

Query Match 100.0%; Score 553; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.2e-51;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125
```

RESULT 2
Q96DS4
ID Q96DS4 PRELIMINARY; PRT; 195 AA.
AC Q96DS4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MDM2 variant FB26.
GN Name=MDM2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Rhabdomyosarcoma tumor;

```
RA   Bartel F., Taylor A.C., Taubert H., Harris L.C.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF385323; AAL13243.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB_MDM2.
DR   Pfam; PF02201; SWIB; 1.
SQ   SEQUENCE   195 AA;  22161 MW;  4987AE567DB12D5D CRC64;

  Query Match             100.0%;  Score 553;  DB 2;  Length 195;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-51;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 3
Q8TE47
ID   Q8TE47      PRELIMINARY;      PRT;   243 AA.
AC   Q8TE47;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   MDM2 isoform KB9 protein.
GN   Name=MDM2 isoform KB9;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymphocytes;
RA   Bartel F., Pinkert D., Kappler M., Bache M., Schmidt H., Taubert H.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ430612; CAD23251.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR   GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   GO; GO:0016567; P:protein ubiquitination; IEA.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB_MDM2.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
SQ   SEQUENCE   243 AA;  27317 MW;  9EB5D0142CF185A2 CRC64;

  Query Match             100.0%;  Score 553;  DB 2;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-51;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 4
MDM2_HUMAN
ID   MDM2_HUMAN     STANDARD;      PRT;   491 AA.
AC   Q00987; Q13226; Q13297; Q13298; Q13299; Q13300; Q13301; Q9UGI3;
AC   Q9UMT8;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein
DE   Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Hdm2).
GN   Name=MDM2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM MDM2).
RX   MEDLINE=92310576; PubMed=1614537;
RA   Oliner J.D., Kinzler K.W., Meltzer P.S., George D.L., Vogelstein B.;
RT   "Amplification of a gene encoding a p53-associated protein in human
RT   sarcomas.";
RL   Nature 358:80-83(1992).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS MDM2-A; -B; -C; -D AND -E).
RC   TISSUE=Ovarian carcinoma;
RX   MEDLINE=96313107; PubMed=8705862;
RA   Sigalas I., Calvert A.H., Anderson J.J., Neal D.E., Lunec J.;
RT   "Alternatively spliced mdm2 transcripts with loss of p53 binding
RT   domain sequences: transforming ability and frequent detection in human
RT   cancer.";
RL   Nat. Med. 2:912-917(1996).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM MDM2-ALPHA).
RX   MEDLINE=20065171; PubMed=10597303;
RA   Veldhoen N., Metcalfe S., Milner J.;
RT   "A novel exon within the mdm2 gene modulates translation initiation in
RT   vitro and disrupts the p53-binding domain of mdm2 protein.";
RL   Oncogene 18:7026-7033(1999).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM MDM2).
RA   Rieder M.J., Livingston R.J., Braun A.C., Montoya M.A., Chung M.-W.,
RA   Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA   Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RT   "NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department
RT   of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM MDM2).
RC   TISSUE=Muscle;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [6]
RP   SEQUENCE OF 6-491 FROM N.A. (ISOFORM MDM2-A1).
RA   Liang H., Atkins H., Abdel-Fattah R., Suaeyun R., Lunec J.;
RT   "Genomic organisation of the human MDM2 oncogene and relationship to
RT   its alternatively spliced mRNA's.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
RN   [7]
```

```
RP   SEQUENCE OF 1-24 FROM N.A.
RX   MEDLINE=95380270; PubMed=7651818;
RA   Zauberman A., Flusberg D., Haupt Y., Barak Y., Oren M.;
RT   "A functional p53-responsive intronic promoter is contained within the
RT   human mdm2 gene.";
RL   Nucleic Acids Res. 23:2584-2592(1995).
RN   [8]
RP   SEQUENCE OF 1-9 FROM N.A.
RX   MEDLINE=97413643; PubMed=9270029;
RA   Landers J.E., Cassel S.L., George D.L.;
RT   "Translational enhancement of mdm2 oncogene expression in human tumor
RT   cells containing a stabilized wild-type p53 protein.";
RL   Cancer Res. 57:3562-3568(1997).
RN   [9]
RP   SEQUENCE OF 301-481 FROM N.A.
RX   MEDLINE=20542019; PubMed=11087894;
RA   Taubert H., Kappler M., Meye A., Bartel F., Schlott T.,
RA   Lautenschlaeger C., Bache M., Schmidt H., Wuerl P.;
RT   "A MboII polymorphism in exon 11 of the human MDM2 gene occuring in
RT   normal blood donors and in soft tissue sarcoma patients: an indication
RT   for an increased cancer susceptibility?";
RL   Mutat. Res. 456:39-44(2000).
RN   [10]
RP   MUTAGENESIS OF CYS-464.
RX   MEDLINE=98111004; PubMed=9450543;
RA   Honda R., Tanaka H., Yasuda H.;
RT   "Oncoprotein MDM2 is a ubiquitin ligase E3 for tumor suppressor p53.";
RL   FEBS Lett. 420:25-27(1997).
RN   [11]
RP   MUTAGENESIS OF CYS-449.
RX   MEDLINE=20190101; PubMed=10723139;
RA   Honda R., Yasuda H.;
RT   "Activity of MDM2, a ubiquitin ligase, toward p53 or itself is
RT   dependent on the RING finger domain of the ligase.";
RL   Oncogene 19:1473-1476(2000).
RN   [12]
RP   MUTAGENESIS.
RX   MEDLINE=20187618; PubMed=10722742;
RA   Fang S., Jensen J.P., Ludwig R.L., Vousden K.H., Weissman A.M.;
RT   "Mdm2 is a RING finger-dependent ubiquitin protein ligase for itself
RT   and p53.";
RL   J. Biol. Chem. 275:8945-8951(2000).
RN   [13]
RP   MUTAGENESIS OF CYS-441 AND CYS-478.
RX   MEDLINE=20076498; PubMed=10608892;
RA   Sharp D.A., Kratowicz S.A., Sank M.J., George D.L.;
RT   "Stabilization of the MDM2 oncoprotein by interaction with the
RT   structurally related MDMX protein.";
RL   J. Biol. Chem. 274:38189-38196(1999).
RN   [14]
RP   NUCLEOLAR LOCALIZATION SIGNAL.
RX   MEDLINE=20173879; PubMed=10707090;
RA   Lohrum M.A.E., Ashcroft M., Kubbutat M.H.G., Vousden K.H.;
RT   "Identification of a cryptic nucleolar-localization signal in MDM2.";
RL   Nat. Cell Biol. 2:179-181(2000).
RN   [15]
RP   PHOSPHORYLATION BY ATM.
RX   MEDLINE=20079591; PubMed=10611322;
RA   Khosravi R., Maya R., Gottlieb T., Oren M., Shiloh Y., Shkedy D.;
RT   "Rapid ATM-dependent phosphorylation of MDM2 precedes p53 accumulation
RT   in response to DNA damage.";
RL   Proc. Natl. Acad. Sci. U.S.A. 96:14973-14977(1999).
RN   [16]
RP   X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 25-109 IN COMPLEX WITH P53.
RX   MEDLINE=97081050; PubMed=8875929;
RA   Kussie P.H., Gorina S., Marechal V., Elenbaas B., Moreau J.,
RA   Levine A.J., Pavletich N.P.;
RT   "Structure of the MDM2 oncoprotein bound to the p53 tumor suppressor
RT   transactivation domain.";
RL   Science 274:948-953(1996).
CC   -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC       apoptosis by binding its transcriptional activation domain.
CC       Functions as a ubiquitin ligase E3, in the presence of E1 and E2,
CC       toward p53 and itself. Permits the nuclear export of p53 and
CC       targets it for proteasome-mediated proteolysis.
CC   -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity.
CC   -!- SUBUNIT: Binds p53, p73, ARF(P14), ribosomal protein L5 and
CC       specifically to RNA. Can interact also with retinoblastoma protein
CC       (RB), E1A-associated protein EP300 and the E2F1 transcription
CC       factor.
CC   -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed
CC       predominantly in the nucleoplasm. Interaction with ARF(P14)
CC       results in the localization of both proteins to the nucleolus. The
CC       nucleolar localization signals in both ARF(P14) and MDM2 may be
CC       necessary to allow efficient nucleolar localization of both
CC       proteins.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=8;
CC       Name=Mdm2;
CC         IsoId=Q00987-1; Sequence=Displayed;
CC       Name=Mdm2-A;
CC         IsoId=Q00987-2; Sequence=VSP_003208;
CC       Name=Mdm2-A1;
CC         IsoId=Q00987-3; Sequence=VSP_003208, VSP_003214;
CC       Name=Mdm2-B;
CC         IsoId=Q00987-4; Sequence=VSP_003209;
CC       Name=Mdm2-C;
CC         IsoId=Q00987-5; Sequence=VSP_003211;
CC       Name=Mdm2-D;
CC         IsoId=Q00987-6; Sequence=VSP_003210;
CC       Name=Mdm2-E;
CC         IsoId=Q00987-7; Sequence=VSP_003212, VSP_003213;
CC       Name=Mdm2-alpha;
CC         IsoId=Q00987-8; Sequence=VSP_003207;
CC   -!- TISSUE SPECIFICITY: Ubiquitous. Isoforms MDM2-A, -B, -C, -D and -E
CC       are observed in a range of human cancers but absent in normal
CC       tissues.
CC   -!- INDUCTION: By DNA damage.
CC   -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its
CC       G1 arrest and apoptosis functions. It also binds p73 and E2F1.
CC       Region II contains most of a central acidic region required for
CC       interaction with ribosomal protein L5 and a putative C4-type zinc
CC       finger. The RING finger domain which coordinates two molecules of
CC       zinc interacts specifically with RNA whether or not zinc is
CC       present and mediates the hetero-oligomerization with MDM4. It is
CC       also essential for its ubiquitin ligase E3 activity toward p53 and
CC       itself.
CC   -!- PTM: Phosphorylated in response to ionizing radiation in an ATM-
CC       dependent manner.
CC   -!- DISEASE: Seems to be amplified in certain tumors (including soft
CC       tissue sarcomas, osteosarcomas and gliomas). A higher frequency of
CC       splice variants lacking p53 binding domain sequences was found in
CC       late-stage and high-grade ovarian and bladder carcinomas. Four of
CC       the splice variants show loss of p53 binding.
CC   -!- MISCELLANEOUS: MDM2 RING finger mutations that failed to

  Query Match           100.0%;  Score 553;  DB 1;  Length 491;
  Best Local Similarity  100.0%;  Pred. No. 4e-51;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 5
AAP35922
ID   AAP35922    PRELIMINARY;      PRT;   491 AA.
AC   AAP35922;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
```

```
DE   Mdm2, transformed 3T3 cell double minute 2, p53 binding protein
DE   (Mouse).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA   Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA   Phelan M., Farmer A.;
RT   "Cloning of human full-length CDSs in BD Creator(TM) System Donor
RT   vector.";
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BT007258; AAP35922.1; -.
SQ   SEQUENCE   491 AA;  55232 MW;  F37CE163876BC983 CRC64;

  Query Match             100.0%;  Score 553;  DB 2;  Length 491;
  Best Local Similarity   100.0%;  Pred. No. 4e-51;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 6
AAH67077
ID   AAH67077    PRELIMINARY;      PRT;   491 AA.
AC   AAH67077;
DT   14-APR-2004 (TrEMBLrel. 27, Created)
DT   14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT   14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle;
RA   Strausberg R.;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC067077; AAH67077.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   491 AA;  55232 MW;  F37CE163876BC983 CRC64;

  Query Match             100.0%;  Score 553;  DB 2;  Length 491;
  Best Local Similarity   100.0%;  Pred. No. 4e-51;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 7
MDM2_CANFA
ID   MDM2_CANFA     STANDARD;      PRT;   487 AA.
AC   P56950; Q95KN5;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein
DE   Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Cdm2).
GN   Name=MDM2;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE OF 1-484 FROM N.A.
RX   MEDLINE=20218866; PubMed=10754200;
RA   Nasir L., Burr P.D., McFarlane S.T., Gault E., Thompson H.,
RA   Argyle D.J.;
RT   "Cloning, sequence analysis and expression of the cDNAs encoding the
RT   canine and equine homologues of the mouse double minute 2 (mdm2)
RT   proto-oncogene.";
RL   Cancer Lett. 152:9-13(2000).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS MDM2 AND MDM2-ALPHA).
RX   MEDLINE=20065171; PubMed=10597303;
RA   Veldhoen N., Metcalfe S., Milner J.;
RT   "A novel exon within the mdm2 gene modulates translation initiation in
RT   vitro and disrupts the p53-binding domain of mdm2 protein.";
RL   Oncogene 18:7026-7033(1999).
CC   -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC       apoptosis by binding its transcriptional activation domain.
CC       Functions as a ubiquitin ligase E3, in the presence of E1 and E2,
CC       toward p53 and itself. Permits the nuclear export of p53 and
CC       targets it for proteasome-mediated proteolysis (By similarity).
CC   -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity (By
CC       similarity).
CC   -!- SUBUNIT: Binds p53, p73, ARF(P14), ribosomal protein L5 and
CC       specifically to RNA. Can interact also with retinoblastoma protein
CC       (RB), E1A-associated protein EP300 and the E2F1 transcription
CC       factor (By similarity).
CC   -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed
CC       predominantly in the nucleoplasm (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Mdm2;
CC         IsoId=P56950-1; Sequence=Displayed;
CC       Name=Mdm2-alpha;
CC         IsoId=P56950-2; Sequence=VSP_003206;
CC   -!- TISSUE SPECIFICITY: Isoform Mdm2-alpha is present in lymphoid and
CC       testicular tissues.
CC   -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its
CC       G1 arrest and apoptosis functions. It also binds p73 and E2F1.
CC       Region II contains most of a central acidic region required for
CC       interaction with ribosomal protein L5 and a putative C4-type zinc
CC       finger. The RING finger domain which coordinates two molecules of
CC       zinc interacts specifically with RNA whether or not zinc is
CC       present and mediates the hetero-oligomerization with MDM4. It is
```

```
CC       also essential for its ubiquitin ligase E3 activity toward p53 and
CC       itself (By similarity).
CC   -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.
CC   -!- SIMILARITY: Contains 1 RanBP2-type zinc finger.
CC   -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC   -!- SIMILARITY: Contains 1 SWIB domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF100705; AAF67833.1; -.
DR   EMBL; AF322416; AAG42840.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Alternative splicing; Ligase; Metal-binding; Nuclear protein;
KW   Ubl conjugation pathway; Zinc; Zinc-finger.
FT   DOMAIN       27    107       SWIB.
FT   DOMAIN      179    185       Nuclear localization signal (Potential).
FT   DOMAIN      190    202       Nuclear export signal.
FT   DOMAIN      210    304       ARF-binding.
FT   DOMAIN      210    215       Poly-Ser.
FT   DOMAIN      242    331       Region II.
FT   DOMAIN      243    301       Asp/Glu-rich (acidic).
FT   ZN_FING     299    328       RanBP2-type.
FT   ZN_FING     434    475       RING-type.
FT   DOMAIN      462    469       Nucleolar localization signal
FT                                (Potential).
FT   VARSPLIC      1     61       Missing (in isoform Mdm2-alpha).
FT                                /FTId=VSP_003206.
FT   CONFLICT     11     11       G -> D (in Ref. 2).
FT   CONFLICT    238    239       QD -> HH (in Ref. 2).
SQ   SEQUENCE   487 AA;  54696 MW;  60CDB470A32A8E69 CRC64;

  Query Match             97.8%;  Score 541;  DB 1;  Length 487;
  Best Local Similarity   97.2%;  Pred. No. 7.9e-50;
  Matches  106;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVIFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||||||||||||||| | ||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQHEPSDSGTSVSEN 125


RESULT 8
Q9GMZ6
ID   Q9GMZ6      PRELIMINARY;      PRT;   487 AA.
AC   Q9GMZ6;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   MDM2.
GN   Name=mdm2;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Setoguchi A., Tsujimoto H.;
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB031276; BAB11975.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   GO; GO:0005730; C:nucleolus; ISS.
DR   GO; GO:0005654; C:nucleoplasm; ISS.
DR   GO; GO:0017163; F:negative regulator of basal transcription a. . .; ISS.
DR   GO; GO:0005515; F:protein binding; ISS.
DR   GO; GO:0000122; P:negative regulation of transcription from P. . .; ISS.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB_MDM2.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
SQ   SEQUENCE   487 AA;  54724 MW;  34FC5CC6A18D7744 CRC64;

  Query Match             97.8%;  Score 541;  DB 2;  Length 487;
  Best Local Similarity   97.2%;  Pred. No. 7.9e-50;
  Matches  106;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVIFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||||||||||||||| | ||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQHEPSDSGTSVSEN 125


RESULT 9
MDM2_HORSE
ID   MDM2_HORSE     STANDARD;      PRT;   491 AA.
AC   P56951;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein
DE   Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Edm2).
GN   Name=MDM2;
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20218866; PubMed=10754200;
RA   Nasir L., Burr P.D., McFarlane S.T., Gault E., Thompson H.,
RA   Argyle D.J.;
RT   "Cloning, sequence analysis and expression of the cDNAs encoding the
RT   canine and equine homologues of the mouse double minute 2 (mdm2)
RT   proto-oncogene.";
RL   Cancer Lett. 152:9-13(2000).
CC   -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC       apoptosis by binding its transcriptional activation domain.
CC       Functions as a ubiquitin ligase E3, in the presence of E1 and E2,
CC       toward p53 and itself. Permits the nuclear export of p53 and
CC       targets it for proteasome-mediated proteolysis (By similarity).
CC   -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity (By
CC       similarity).
CC   -!- SUBUNIT: Binds p53, p73, ARF(P14), ribosomal protein L5 and
CC       specifically to RNA. Can interact also with retinoblastoma protein
CC       (RB), E1A-associated protein EP300 and the E2F1 transcription
CC       factor (By similarity).
CC   -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed
```

```
CC       predominantly in the nucleoplasm (By similarity).
CC   -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its
CC       G1 arrest and apoptosis functions. It also binds p73 and E2F1.
CC       Region II contains most of a central acidic region required for
CC       interaction with ribosomal protein L5 and a putative C4-type zinc
CC       finger. The RING finger domain which coordinates two molecules of
CC       zinc interacts specifically with RNA whether or not zinc is
CC       present and mediates the hetero-oligomerization with MDM4. It is
CC       also essential for its ubiquitin ligase E3 activity toward p53 and
CC       itself (By similarity).
CC   -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.
CC   -!- SIMILARITY: Contains 1 RanBP2-type zinc finger.
CC   -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC   -!- SIMILARITY: Contains 1 SWIB domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF121140; AAF28866.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Ligase; Metal-binding; Nuclear protein; Ubl conjugation pathway; Zinc;
KW   Zinc-finger.
FT   DOMAIN       27    107       SWIB.
FT   DOMAIN      179    185       Nuclear localization signal (Potential).
FT   DOMAIN      190    202       Nuclear export signal.
FT   DOMAIN      210    304       ARF-binding.
FT   DOMAIN      210    215       Poly-Ser.
FT   DOMAIN      242    331       Region II.
FT   DOMAIN      243    301       Asp/Glu-rich (acidic).
FT   ZN_FING     299    328       RanBP2-type.
FT   ZN_FING     438    479       RING-type.
FT   DOMAIN      466    473       Nucleolar localization signal
FT                                (Potential).
SQ   SEQUENCE   491 AA;  55279 MW;  641E033D5C1DEC39 CRC64;

  Query Match             97.8%;  Score 541;  DB 1;  Length 491;
  Best Local Similarity   97.2%;  Pred. No. 8e-50;
  Matches  106;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVIFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||||||||||||:||| ||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVSQQEPSDSGTSVSEN 125


RESULT 10
Q7YRZ8
ID   Q7YRZ8       PRELIMINARY;      PRT;   491 AA.
AC   Q7YRZ8;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Double minute 2 protein MDM2.
GN   Name=mdm2;
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Miki R., Okuda M., Ma Z., Inokuma H., Onishi T.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB099709; BAC78209.1; -.
DR   GO; GO:0005730; C:nucleolus; ISS.
DR   GO; GO:0005654; C:nucleoplasm; ISS.
DR   GO; GO:0017163; F:negative regulator of basal transcription a. . .; ISS.
DR   GO; GO:0005515; F:protein binding; ISS.
DR   GO; GO:0000122; P:negative regulation of transcription from P. . .; ISS.
DR   InterPro; IPR003121; SWIB_MDM2.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
SQ   SEQUENCE   491 AA;  55433 MW;  D93E25D638E88934 CRC64;

  Query Match             97.3%;  Score 538;  DB 2;  Length 491;
  Best Local Similarity   96.3%;  Pred. No. 1.7e-49;
  Matches  105;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||:||||||||||||||||||||||||||||||||:||||||||||||||||||||||||
Db         17 SQMPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVIFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||| | ||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQHEPSDSGTSVSEN 125


RESULT 11
Q8WYJ2
ID   Q8WYJ2       PRELIMINARY;      PRT;   436 AA.
AC   Q8WYJ2;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   MDM2 protein.
GN   Name=MDM2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21248713; PubMed=11351297;
RA   Tamborini E., Della Torre G., Lavarino C., Azzarelli A.,
RA   Carpinelli P., Pierotti M.A., Pilotti S.;
RT   "Analysis of the molecular species generated by MDM2 gene
RT   amplification in liposarcomas.";
RL   Int. J. Cancer 92:790-796(2001).
DR   EMBL; AF092844; AAL40179.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   GO; GO:0005730; C:nucleolus; ISS.
DR   GO; GO:0005654; C:nucleoplasm; ISS.
DR   GO; GO:0017163; F:negative regulator of basal transcription a. . .; ISS.
DR   GO; GO:0005515; F:protein binding; ISS.
DR   GO; GO:0000122; P:negative regulation of transcription from P. . .; ISS.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB_MDM2.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
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DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
SQ   SEQUENCE   436 AA;  49248 MW;  3C8F55E98BC4203A CRC64;

  Query Match           91.0%;  Score 503;  DB 2;  Length 436;
  Best Local Similarity   94.3%;  Pred. No. 9.1e-46;
  Matches   99;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTS 105
              |||||||||||||||||||||||||||||||||||| :    |
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQEENSDELS 121


RESULT 12
MDM2_MOUSE
ID   MDM2_MOUSE     STANDARD;      PRT;   489 AA.
AC   P23804; Q61040; Q64330;
DT   01-NOV-1991 (Rel. 20, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein
DE   Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein).
GN   Name=Mdm2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM MDM2-P90).
RX   MEDLINE=91224107; PubMed=2026149;
RA   Fakharzadeh S.S., Trusko S.P., George D.L.;
RT   "Tumorigenic potential associated with enhanced expression of a gene
RT   that is amplified in a mouse tumor cell line.";
RL   EMBO J. 10:1565-1569(1991).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM MDM2-P90).
RC   STRAIN=129/Sv;
RX   MEDLINE=97074674; PubMed=8917101;
RA   Jones S.N., Ansari-Lari M.A., Hancock A.R., Jones W.J., Gibbs R.A.,
RA   Donehower L.A., Bradley A.;
RT   "Genomic organization of the mouse double minute 2 gene.";
RL   Gene 175:209-213(1996).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM MDM2-P90).
RC   STRAIN=129/Sv;
RX   MEDLINE=96299630; PubMed=8660994;
RA   de Oca Luna R.M., Tabor A.D., Eberspaecher H., Hulboy D.L.,
RA   Worth L.L., Colman M.S., Finlay C.A., Lozano G.;
RT   "The organization and expression of the mdm2 gene.";
RL   Genomics 33:352-357(1996).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORMS MDM2-P90 AND MDM2-P76).
RX   MEDLINE=99175199; PubMed=10075719;
RA   Saucedo L.J., Myers C.D., Perry M.E.;
RT   "Multiple murine double minute gene 2 (MDM2) proteins are induced by
RT   ultraviolet light.";
RL   J. Biol. Chem. 274:8161-8168(1999).
RN   [5]
RP   NUCLEOLAR LOCALIZATION SIGNAL.
RX   MEDLINE=20180080; PubMed=10713175;
RA   Weber J.D., Kuo M.-L., Bothner B., DiGiammarino E.L., Kriwacki R.W.,
RA   Roussel M.F., Sherr C.J.;
RT   "Cooperative signals governing ARF-mdm2 interaction and nucleolar
RT   localization of the complex.";
RL   Mol. Cell. Biol. 20:2517-2528(2000).
RN   [6]
RP   PHOSPHORYLATION BY ATM.
RX   MEDLINE=20079591; PubMed=10611322;
RA   Khosravi R., Maya R., Gottlieb T., Oren M., Shiloh Y., Shkedy D.;
RT   "Rapid ATM-dependent phosphorylation of MDM2 precedes p53 accumulation
RT   in response to DNA damage.";
RL   Proc. Natl. Acad. Sci. U.S.A. 96:14973-14977(1999).
CC   -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC       apoptosis by binding its transcriptional activation domain.
CC       Functions as a ubiquitin ligase E3, in the presence of E1 and E2,
CC       toward p53 and itself. Permits the nuclear export of p53 and
CC       targets it for proteasome-mediated proteolysis.
CC   -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity.
CC   -!- SUBUNIT: Binds p53, p73, ARF(P14), ribosomal protein L5 and
CC       specifically to RNA. Can interact also with retinoblastoma protein
CC       (RB), E1A-associated protein EP300 and the E2F1 transcription
CC       factor.
CC   -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed
CC       predominantly in the nucleoplasm. Interaction with ARF(P14)
CC       results in the localization of both proteins to the nucleolus. The
CC       nucleolar localization signals in both ARF(P14) and MDM2 may be
CC       necessary to allow efficient nucleolar localization of both
CC       proteins.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Mdm2-p90;
CC         IsoId=P23804-1; Sequence=Displayed;
CC         Note=Isoform Mdm2-p76 can also be produced by alternative
CC         initiation at Met-50 of isoform Mdm2-p90, but is produced more
CC         efficiently by alternative splicing;
CC       Name=Mdm2-p76;
CC         IsoId=P23804-2; Sequence=VSP_003215;
CC         Note=Does not bind to p53;
CC       Event=Alternative initiation;
CC         Comment=2 isoforms, Mdm2-p90 (shown here) and Mdm2-p76, are
CC         produced by alternative initiation at Met-1 and Met-50. Isoform
CC         Mdm2-p76 is produced more efficiently by alternative splicing;
CC   -!- TISSUE SPECIFICITY: Ubiquitously expressed at low-level throughout
CC       embryo development and in adult tissues. MDM2-p90 is much more
CC       abundant than MDM2-p76 in testis, brain, heart, and kidney, but in
CC       the thymus, spleen, and intestine, the levels of the MDM2 proteins
CC       are roughly equivalent.
CC   -!- INDUCTION: By UV light.
CC   -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its
CC       G1 arrest and apoptosis functions. It also binds p73 and E2F1.
CC       Region II contains most of a central acidic region required for
CC       interaction with ribosomal protein L5 and a putative C4-type zinc
CC       finger. The RING finger domain which coordinates two molecules of
CC       zinc interacts specifically with RNA whether or not zinc is
CC       present and mediates the hetero-oligomerization with MDM4. It is
CC       also essential for its ubiquitin ligase E3 activity toward p53 and
CC       itself.
CC   -!- PTM: Phosphorylated in response to ionizing radiation in an ATM-
CC       dependent manner.
CC   -!- DISEASE: The gene for this protein is amplified in a mouse tumor
CC       cell line.
CC   -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.
CC   -!- SIMILARITY: Contains 1 RanBP2-type zinc finger.
CC   -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC   -!- SIMILARITY: Contains 1 SWIB domain.
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; X58876; CAA41684.1; -.
DR   EMBL; U40145; AAA91167.1; -.
DR   EMBL; U47944; AAB09030.1; -.
DR   EMBL; U47935; AAB09030.1; JOINED.
DR   EMBL; U47936; AAB09030.1; JOINED.
DR   EMBL; U47937; AAB09030.1; JOINED.
DR   EMBL; U47938; AAB09030.1; JOINED.
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DR   EMBL; U47939; AAB09030.1; JOINED.
DR   EMBL; U47940; AAB09030.1; JOINED.
DR   EMBL; U47941; AAB09030.1; JOINED.
DR   EMBL; U47942; AAB09030.1; JOINED.
DR   EMBL; U47943; AAB09030.1; JOINED.
DR   EMBL; U47934; AAB09031.1; -.
DR   PIR; S15349; S15349.
DR   HSSP; Q9UMT8; 1YCR.
DR   MGD; MGI:96952; Mdm2.
DR   GO; GO:0005634; C:nucleus; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0004842; F:ubiquitin-protein ligase activity; IDA.
DR   GO; GO:0030163; P:protein catabolism; IDA.
DR   GO; GO:0016567; P:protein ubiquitination; IDA.
DR   GO; GO:0007089; P:traversing start control point of mitotic c. . .; IDA.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Alternative initiation; Alternative splicing; Ligase; Metal-binding;
KW   Nuclear protein; Phosphorylation; Proto-oncogene;
KW   Ubl conjugation pathway; Zinc; Zinc-finger.
FT   CHAIN         1    489       Ubiquitin-protein ligase E3 Mdm2, isoform
FT                                Mdm2-p90.
FT   CHAIN        50    489       ubiquitin-protein ligase E3 Mdm2, isoform
FT                                Mdm2-p76.
FT   INIT_MET     50     50       For isoform Mdm2-p76.
FT   DOMAIN       27    107       SWIB.
FT   DOMAIN      176    182       Nuclear localization signal (Potential).
FT   DOMAIN      183    195       Nuclear export signal.
FT   DOMAIN      203    213       Poly-Ser.
FT   DOMAIN      208    302       ARF-binding.
FT   DOMAIN      240    329       Region II.
FT   DOMAIN      221    299       Asp/Glu-rich (acidic).
FT   ZN_FING     297    326       RanBP2-type.
FT   ZN_FING     436    477       RING-type.
FT   DOMAIN      464    471       Nucleolar localization signal
FT                                (Potential).
FT   VARSPLIC      1     49       Missing (in isoform Mdm2-p76).
FT                                /FTId=VSP_003215.
FT   CONFLICT    203    203       S -> T (in Ref. 1).
FT   CONFLICT    419    419       D -> H (in Ref. 1).
FT   CONFLICT    486    486       S -> T (in Ref. 3).
SQ   SEQUENCE   489 AA;  54543 MW;  4ABF489E92038DF4 CRC64;

  Query Match             89.2%;  Score 493.5;  DB 1;  Length 489;
  Best Local Similarity   88.1%;  Pred. No. 1.1e-44;
  Matches   96;  Conservative    7;  Mismatches    3;  Indels    3;  Gaps    1;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              |||||||||||||||||||||||||||| ||||||::||:||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQNDTYTMKEIIFYIGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||:|||||||||||||||| ||||||| |:||   |||||:||:
Db         77 CSNDLLGDVFGVPSFSVKEHRKIYAMIYRNLVAVSQQ---DSGTSLSES 122


RESULT 13
Q91XK7
ID   Q91XK7      PRELIMINARY;      PRT;   489 AA.
AC   Q91XK7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Mus musculus adult male lung cDNA, RIKEN full-length enriched library,
DE   clone:1200011P22 product:transformed mouse 3T3 cell double minute 2,
DE   full insert sequence (Transformed mouse 3T3 cell double minute 2) (Mus
DE   musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length
DE   enriched library, clone:E430022B10 product:transformed mouse 3T3 cell
DE   double minute 2, full insert sequence).
GN   Name=Mdm2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;
RX   MEDLINE=99279253; PubMed=10349636;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;
RX   MEDLINE=21085660; PubMed=11217851;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;
RX   MEDLINE=20499374; PubMed=11042159;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;
RX   MEDLINE=20530913; PubMed=11076861;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Lung;
RA   Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA   Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA   Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA   Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA   Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA   Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA   Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA   Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA   Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA   Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Mouse;
```

```
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [8]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Mouse;
RA   Strausberg R.;
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
RN   [9]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NOD; TISSUE=Thymus;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK004719; BAB23502.1; -.
DR   EMBL; BC050902; AAH50902.1; -.
DR   EMBL; AK088638; BAC40470.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   MGD; MGI:96952; Mdm2.
DR   GO; GO:0005730; C:nucleolus; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0004842; F:ubiquitin-protein ligase activity; IDA.
DR   GO; GO:0030163; P:protein catabolism; IDA.
DR   GO; GO:0016567; P:protein ubiquitination; IDA.
DR   GO; GO:0007089; P:traversing start control point of mitotic c. . .; IDA.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB_MDM2.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
SQ   SEQUENCE   489 AA;  54557 MW;  4ABF489A82038DF4 CRC64;

  Query Match             89.2%;  Score 493.5;  DB 2;  Length 489;
  Best Local Similarity   88.1%;  Pred. No. 1.1e-44;
  Matches   96;  Conservative    7;  Mismatches    3;  Indels    3;  Gaps    1;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
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Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQNDTYTMKEIIFYIGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||:|||||||||||||| ||||||| |:||   |||||:||:
Db         77 CSNDLLGDVFGVPSFSVKEHRKIYAMIYRNLVAVSQQ---DSGTSLSES 122


RESULT 14
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ID   Q8WYJ3      PRELIMINARY;      PRT;   118 AA.
AC   Q8WYJ3;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   MDM2 protein (Fragment).
GN   Name=MDM2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21248713; PubMed=11351297;
RA   Tamborini E., Della Torre G., Lavarino C., Azzarelli A.,
RA   Carpinelli P., Pierotti M.A., Pilotti S.;
RT   "Analysis of the molecular species generated by MDM2 gene
RT   amplification in liposarcomas.";
RL   Int. J. Cancer 92:790-796(2001).
DR   EMBL; AF092843; AAL40178.1; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB_MDM2.
DR   Pfam; PF02201; SWIB; 1.
FT   NON_TER     118    118
SQ   SEQUENCE   118 AA;  13536 MW;  D7A4DBAA83D8841B CRC64;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVV 93
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RESULT 15
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ID   MDM2_MESAU     STANDARD;      PRT;   466 AA.
AC   Q60524;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein
DE   Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Fragment).
GN   Name=MDM2;
OS   Mesocricetus auratus (Golden hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC   Mesocricetus.
OX   NCBI_TaxID=10036;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pancreas;
RX   MEDLINE=95300112; PubMed=7780969;
RA   Chang K.W., Laconi S., Mangold K.A., Hubchak S., Scarpelli D.G.;
RT   "Multiple genetic alterations in hamster pancreatic ductal
RT   adenocarcinomas.";
RL   Cancer Res. 55:2560-2568(1995).
CC   -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC       apoptosis by binding its transcriptional activation domain.
CC       Functions as a ubiquitin ligase E3, in the presence of E1 and E2,
CC       toward p53 and itself. Permits the nuclear export of p53 and
```

```
CC       targets it for proteasome-mediated proteolysis (By similarity).
CC   -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity (By
CC       similarity).
CC   -!- SUBUNIT: Binds p53, p73, ARF(P14), ribosomal protein L5 and
CC       specifically to RNA. Can interact also with retinoblastoma protein
CC       (RB), E1A-associated protein EP300 and the E2F1 transcription
CC       factor (By similarity).
CC   -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed
CC       predominantly in the nucleoplasm (By similarity).
CC   -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its
CC       G1 arrest and apoptosis functions. It also binds p73 and E2F1.
CC       Region II contains most of a central acidic region required for
CC       interaction with ribosomal protein L5 and a putative C4-type zinc
CC       finger. The RING finger domain which coordinates two molecules of
CC       zinc interacts specifically with RNA whether or not zinc is
CC       present and mediates the hetero-oligomerization with MDM4. It is
CC       also essential for its ubiquitin ligase E3 activity toward p53 and
CC       itself (By similarity).
CC   -!- DISEASE: The gene for this protein is overexpressed in some
CC       tumors.
CC   -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.
CC   -!- SIMILARITY: Contains 1 RanBP2-type zinc finger.
CC   -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC   -!- SIMILARITY: Contains 1 SWIB domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U10982; AAC52425.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Ligase; Metal-binding; Nuclear protein; Proto-oncogene;
KW   Ubl conjugation pathway; Zinc; Zinc-finger.
FT   NON_TER       1      1
FT   DOMAIN       19     98       SWIB.
FT   DOMAIN      169    175       Nuclear localization signal (Potential).
FT   DOMAIN      176    188       Nuclear export signal.
FT   DOMAIN      196    201       Poly-Ser.
FT   DOMAIN      196    290       ARF-binding.
FT   DOMAIN      228    317       Region II.
FT   DOMAIN      209    287       Asp/Glu-rich (acidic).
FT   ZN_FING     285    314       RanBP2-type.
FT   ZN_FING     419    460       RING-type.
FT   DOMAIN      447    454       Nucleolar localization signal
FT                                (Potential).
FT   NON_TER     466    466
SQ   SEQUENCE   466 AA;  52390 MW;  78A3042163C5F939 CRC64;

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Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
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Search completed: January 27, 2005, 18:13:23
Job time : 86.6 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:54:26 ; Search time 22.2 Seconds
(without alignments)
325.615 Million cell updates/sec

Title: US-10-822-254-2
Perfect score: 553
Sequence: 1 SQIPASEQETLVRPKPLLLK.....NLVVVNQQESSDSGTSVSEN 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	553	100.0	188	4	US-09-603-052-4	Sequence 4, Appli
2	553	100.0	491	1	US-07-903-103-2	Sequence 2, Appli
3	553	100.0	491	1	US-08-044-619A-2	Sequence 2, Appli
4	553	100.0	491	1	US-08-283-911-2	Sequence 2, Appli
5	553	100.0	491	1	US-08-245-500A-3	Sequence 3, Appli
6	553	100.0	491	1	US-08-390-546-3	Sequence 3, Appli
7	553	100.0	491	1	US-08-390-479A-3	Sequence 3, Appli
8	553	100.0	491	1	US-08-557-393-3	Sequence 3, Appli
9	553	100.0	491	1	US-08-390-516C-3	Sequence 3, Appli
10	553	100.0	491	1	US-08-390-517A-3	Sequence 3, Appli
11	553	100.0	491	1	US-08-390-515A-3	Sequence 3, Appli
12	553	100.0	491	2	US-08-801-718-3	Sequence 3, Appli
13	553	100.0	491	3	US-09-170-159A-3	Sequence 3, Appli
14	553	100.0	491	4	US-09-480-718-44	Sequence 44, Appl
15	536.5	97.0	216	3	US-09-510-252-4	Sequence 4, Appli
16	493.5	89.2	489	1	US-07-903-103-4	Sequence 4, Appli
17	493.5	89.2	489	1	US-08-044-619A-4	Sequence 4, Appli
18	493.5	89.2	489	1	US-08-283-911-4	Sequence 4, Appli
19	493.5	89.2	489	1	US-08-245-500A-5	Sequence 5, Appli
20	493.5	89.2	489	1	US-08-390-546-5	Sequence 5, Appli
21	493.5	89.2	489	1	US-08-390-479A-5	Sequence 5, Appli
22	493.5	89.2	489	1	US-08-557-393-5	Sequence 5, Appli
23	493.5	89.2	489	1	US-08-390-516C-5	Sequence 5, Appli
24	493.5	89.2	489	1	US-08-390-517A-5	Sequence 5, Appli
25	493.5	89.2	489	1	US-08-390-515A-5	Sequence 5, Appli
26	493.5	89.2	489	2	US-08-801-718-5	Sequence 5, Appli
27	493.5	89.2	489	3	US-09-170-159A-5	Sequence 5, Appli
28	493.5	89.2	489	4	US-09-480-718-46	Sequence 46, Appl
29	176	31.8	243	4	US-09-786-702-2	Sequence 2, Appli
30	70.5	12.7	420	4	US-09-270-767-43304	Sequence 43304, A
31	70	12.7	62	4	US-09-248-796A-24446	Sequence 24446, A
32	68.5	12.4	244	4	US-09-543-681A-6675	Sequence 6675, Ap
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34	64.5	11.7	107	3	US-09-187-859-35	Sequence 35, Appl
35	64.5	11.7	107	3	US-09-187-859-36	Sequence 36, Appl
36	64.5	11.7	107	4	US-09-839-542B-35	Sequence 35, Appl
37	64.5	11.7	107	4	US-09-839-542B-36	Sequence 36, Appl
38	64.5	11.7	107	4	US-09-535-852-35	Sequence 35, Appl
39	64.5	11.7	107	4	US-09-535-852-36	Sequence 36, Appl
40	64.5	11.7	108	4	US-09-535-852-54	Sequence 54, Appl
41	64.5	11.7	108	4	US-09-535-852-57	Sequence 57, Appl
42	64.5	11.7	271	3	US-09-134-001C-3549	Sequence 3549, Ap
43	64.5	11.7	485	3	US-08-378-313-25	Sequence 25, Appl
44	64.5	11.7	485	3	US-08-378-313-27	Sequence 27, Appl
45	64.5	11.7	485	3	US-08-378-313-32	Sequence 32, Appl

ALIGNMENTS

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RESULT 1
US-09-603-052-4
; Sequence 4, Application US/09603052
; Patent No. 6492116
; GENERAL INFORMATION:
;  APPLICANT: Chene, Patrick
;  APPLICANT:  Hochkeppel, Heinz-Kurt
;  TITLE OF INVENTION: Assay for identifying inhibitors of the interaction
;  TITLE OF INVENTION:  between proteins p53 and dm2
;  FILE REFERENCE: MEWB26.001C1
;  CURRENT APPLICATION NUMBER: US/09/603,052
;  CURRENT FILING DATE:  2000-06-26
;  PRIOR APPLICATION NUMBER: EP 95810576.9
;  PRIOR FILING DATE: 1995-09-18
;  PRIOR APPLICATION NUMBER: PCT/EP96/03957
;  PRIOR FILING DATE: 1996-09-10
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 188
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-603-052-4

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  Best Local Similarity  100.0%;  Pred. No. 4e-62;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
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Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 2
US-07-903-103-2
; Sequence 2, Application US/07903103
; Patent No. 5411860
;  GENERAL INFORMATION:
;    APPLICANT:  VOGELSTEIN, BERT
;    APPLICANT:  KINZLER, KENNETH
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G ST., N.W.
```

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;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001-4597
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/903,103
;      FILING DATE:  19920623
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/867.840
;      FILING DATE:  07-APR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.40148
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-903-103-2

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  Best Local Similarity   100.0%;  Pred. No. 1.4e-61;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 3
US-08-044-619A-2
; Sequence 2, Application US/08044619A
; Patent No. 5420263
;  GENERAL INFORMATION:
;    APPLICANT:  THE JOHNS HOPKINS UNIVERSITY
;    APPLICANT:  720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G ST., N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001-4597
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/044,619A
;      FILING DATE:  07-APR-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/903,103
;      FILING DATE:  23-JUN-1992
;      APPLICATION NUMBER:  US 07/867.840
;      FILING DATE:  07-APR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.40148
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-044-619A-2

  Query Match             100.0%;  Score 553;  DB 1;  Length 491;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-61;
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Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 4
US-08-283-911-2
; Sequence 2, Application US/08283911
; Patent No. 5519118
;  GENERAL INFORMATION:
;    APPLICANT:  VOGELSTEIN, BERT
;    APPLICANT:  KINZLER, KENNETH
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G ST., N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001-4597
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/283,911
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/903,103
;      FILING DATE:  23-JUN-1992
;      APPLICATION NUMBER:  US 07/867.840
;      FILING DATE:  07-APR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.40148
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-283-911-2

  Query Match             100.0%;  Score 553;  DB 1;  Length 491;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-61;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 5
US-08-245-500A-3
; Sequence 3, Application US/08245500A
; Patent No. 5550023
;  GENERAL INFORMATION:
;    APPLICANT:  BURRELL, MARILEE
;    APPLICANT:  HILL, DAVID E.
;    APPLICANT:  KINZLER, KENNETH W.
;    APPLICANT:  VOGELSTEIN, BERT
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/245,500A
;      FILING DATE:  07-APR-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.42798
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-245-500A-3

  Query Match             100.0%;  Score 553;  DB 1;  Length 491;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-61;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 6
US-08-390-546-3
; Sequence 3, Application US/08390546
; Patent No. 5606044
;  GENERAL INFORMATION:
;    APPLICANT:  BURRELL, MARILEE
;    APPLICANT:  HILL, DAVID E.
;    APPLICANT:  KINZLER, KENNETH W.
;    APPLICANT:  VOGELSTEIN, BERT
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/390,546
;      FILING DATE:  07-APR-1993
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.42798
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-390-546-3

  Query Match             100.0%;  Score 553;  DB 1;  Length 491;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-61;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 7
US-08-390-479A-3
; Sequence 3, Application US/08390479A
; Patent No. 5618921
;  GENERAL INFORMATION:
;    APPLICANT:  BURRELL, MARILEE
;    APPLICANT:  HILL, DAVID E.
;    APPLICANT:  KINZLER, KENNETH W.
;    APPLICANT:  VOGELSTEIN, BERT
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
```

```
;      ADDRESSEE:  BANNER & WITCOFF, LTD.
;      STREET:  1001 G STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/390,479A
;      FILING DATE:  02-FEB-1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.48992
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-390-479A-3

  Query Match             100.0%;  Score 553;  DB 1;  Length 491;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-61;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 8
US-08-557-393-3
; Sequence 3, Application US/08557393
; Patent No. 5702903
;  GENERAL INFORMATION:
;    APPLICANT:  BURRELL, MARILEE
;    APPLICANT:  HILL, DAVID E.
;    APPLICANT:  KINZLER, KENNETH W.
;    APPLICANT:  VOGELSTEIN, BERT
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/557,393
;      FILING DATE:  13-NOV-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/245,500
;      FILING DATE:  18-MAY-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.42798
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-557-393-3

  Query Match             100.0%;  Score 553;  DB 1;  Length 491;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-61;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 9
US-08-390-516C-3
; Sequence 3, Application US/08390516C
; Patent No. 5708136
;  GENERAL INFORMATION:
;    APPLICANT:  BURRELL, MARILEE
;    APPLICANT:  HILL, DAVID E.
;    APPLICANT:  KINZLER, KENNETH W.
;    APPLICANT:  VOGELSTEIN, BERT
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/390,516C
;      FILING DATE:  07-APR-1993
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.42798
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
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US-08-390-516C-3

Query Match 100.0%; Score 553; DB 1; Length 491;
Best Local Similarity 100.0%; Pred. No. 1.4e-61;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125
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RESULT 10
US-08-390-517A-3
; Sequence 3, Application US/08390517A
; Patent No. 5736338
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,517A
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-390-517A-3

Query Match 100.0%; Score 553; DB 1; Length 491;
Best Local Similarity 100.0%; Pred. No. 1.4e-61;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125
```

RESULT 11

US-08-390-515A-3
; Sequence 3, Application US/08390515A
; Patent No. 5756455
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,515A
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-390-515A-3

Query Match 100.0%; Score 553; DB 1; Length 491;
Best Local Similarity 100.0%; Pred. No. 1.4e-61;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125
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RESULT 12
US-08-801-718-3
; Sequence 3, Application US/08801718
; Patent No. 5858976
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.

```
;      COUNTRY:  USA
;      ZIP:  20001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/801,718
;      FILING DATE:  14-FEB-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/390,515
;      FILING DATE:  07-APR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.42798
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-801-718-3

  Query Match             100.0%;  Score 553;  DB 2;  Length 491;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-61;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
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Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 13
US-09-170-159A-3
; Sequence 3, Application US/09170159A
; Patent No. 6399755
;   GENERAL INFORMATION:
;       APPLICANT: BURRELL, MARILEE
;                  HILL, DAVID E.
;                  KINZLER, KENNETH W.
;                  VOGELSTEIN, BERT
;       TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
;                           HUMAN TUMORS
;       NUMBER OF SEQUENCES: 5
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
;            STREET: 1001 G STREET, N.W.
;            CITY: WASHINGTON
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20001
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/170,159A
;            FILING DATE: 13-Oct-1998
;            CLASSIFICATION: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: KAGAN, SARAH A.
;            REGISTRATION NUMBER: 32,141
;            REFERENCE/DOCKET NUMBER: 01107.42798
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-508-9100
;            TELEFAX: 202-508-9299
;            TELEX: 197430 BBMB UT
;   INFORMATION FOR SEQ ID NO: 3:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 491 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-170-159A-3

  Query Match             100.0%;  Score 553;  DB 3;  Length 491;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-61;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 14
US-09-480-718-44
; Sequence 44, Application US/09480718
; Patent No. 6407062
; GENERAL INFORMATION:
;  APPLICANT: Sherr, Charles J
;  APPLICANT: Quelle, Dawn E
;  APPLICANT: Weber, Jason D.
;  APPLICANT: Roussel, Martine F.
;  APPLICANT: Frederique, Zindy
;  TITLE OF INVENTION: ARF-19, A NOVEL REGULATOR OF THE MAMMALIAN CELL CYCLE
;  FILE REFERENCE: 1340-1-023 CIP 1
;  CURRENT APPLICATION NUMBER: US/09/480,718
;  CURRENT FILING DATE: 2000-01-07
;  EARLIER APPLICATION NUMBER: 09/129,855
;  EARLIER FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-480-718-44

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  Best Local Similarity   100.0%;  Pred. No. 1.4e-61;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 15
US-09-510-252-4
; Sequence 4, Application US/09510252
; Patent No. 6372490
; GENERAL INFORMATION:
;  APPLICANT: Nandabalan, Krishnan
;  APPLICANT:  Yang, Meijia
;  APPLICANT:  Schulz, Vincent
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;  APPLICANT:  CuraGen Corporation
;  TITLE OF INVENTION: MDM INTERACTING PROTEIN AND METHODS OF USE THEREOF
;  FILE REFERENCE: 15966-524 MDM US
;  CURRENT APPLICATION NUMBER: US/09/510,252
;  CURRENT FILING DATE:  2000-02-22
;  PRIOR APPLICATION NUMBER: USSN 60/121,192
;  PRIOR FILING DATE: 1999-02-23
;  PRIOR APPLICATION NUMBER: USSN 60/122,643
;  PRIOR FILING DATE: 1999-03-03
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 216
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-510-252-4

  Query Match             97.0%;  Score 536.5;  DB 3;  Length 216;
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Job time : 24.2 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:59:36 ; Search time 69.4 Seconds
(without alignments)
567.443 Million cell updates/sec

Title: US-10-822-254-2
Perfect score: 553
Sequence: 1 SQIPASEQETLVRPKPLLLK.....NLVVVNQQESSDSGTSVSEN 109

Scoring table: BLOSUM62
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Searched: 1608061 seqs, 361289386 residues

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Minimum DB seq length: 0
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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	553	100.0	491	9	US-09-888-077-1	Sequence 1, Appli
2	553	100.0	491	9	US-09-956-425-8	Sequence 8, Appli
3	553	100.0	491	10	US-09-029-327-2	Sequence 2, Appli
4	553	100.0	491	11	US-09-966-724-2	Sequence 2, Appli
5	553	100.0	491	15	US-10-422-536-137	Sequence 137, App
6	553	100.0	491	15	US-10-232-951-35	Sequence 35, Appl
7	553	100.0	491	17	US-10-685-838-1	Sequence 1, Appli
8	553	100.0	491	17	US-10-724-225-2	Sequence 2, Appli
9	553	100.0	491	17	US-10-489-802-8	Sequence 8, Appli
10	553	100.0	491	17	US-10-723-860-2236	Sequence 2236, Ap
11	536.5	97.0	216	13	US-10-057-510-4	Sequence 4, Appli
12	527.5	95.4	522	15	US-10-287-226-380	Sequence 380, App
13	527.5	95.4	522	15	US-10-287-226-382	Sequence 382, App
14	493.5	89.2	489	9	US-09-956-425-6	Sequence 6, Appli
15	493.5	89.2	489	11	US-09-966-724-4	Sequence 4, Appli
16	493.5	89.2	489	17	US-10-489-802-6	Sequence 6, Appli
17	486	87.9	95	17	US-10-685-838-2	Sequence 2, Appli
18	477	86.3	95	17	US-10-685-838-4	Sequence 4, Appli
19	473	85.5	92	17	US-10-685-838-3	Sequence 3, Appli
20	314	56.8	59	14	US-10-211-088-143	Sequence 143, App
21	76	13.7	472	14	US-10-369-493-16585	Sequence 16585, A
22	76	13.7	473	15	US-10-282-122A-45311	Sequence 45311, A
23	76	13.7	967	15	US-10-282-122A-59020	Sequence 59020, A
24	72.5	13.1	578	16	US-10-437-963-174237	Sequence 174237,
25	72	13.0	969	15	US-10-335-977-7409	Sequence 7409, Ap
26	72	13.0	972	15	US-10-335-977-7410	Sequence 7410, Ap
27	70.5	12.7	225	15	US-10-282-122A-52429	Sequence 52429, A
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29	70.5	12.7	422	14	US-10-369-493-7027	Sequence 7027, Ap
30	70	12.7	613	16	US-10-437-963-113326	Sequence 113326,
31	69.5	12.6	277	15	US-10-282-122A-75363	Sequence 75363, A
32	68.5	12.4	291	15	US-10-425-114-59572	Sequence 59572, A
33	68.5	12.4	291	17	US-10-425-115-191465	Sequence 191465,
34	68.5	12.4	709	15	US-10-282-122A-63455	Sequence 63455, A
35	68	12.3	3092	9	US-09-801-368-172	Sequence 172, App
36	68	12.3	3092	14	US-10-369-493-1470	Sequence 1470, Ap
37	67.5	12.2	438	10	US-09-769-787-48	Sequence 48, Appl
38	67.5	12.2	467	14	US-10-362-774-3	Sequence 3, Appli
39	67.5	12.2	467	14	US-10-369-493-6071	Sequence 6071, Ap
40	67	12.1	404	15	US-10-282-122A-61064	Sequence 61064, A
41	67	12.1	701	15	US-10-282-122A-53065	Sequence 53065, A
42	67	12.1	1031	16	US-10-437-963-189155	Sequence 189155,
43	66.5	12.0	498	14	US-10-369-493-20438	Sequence 20438, A
44	66.5	12.0	839	14	US-10-295-027-326	Sequence 326, App
45	66.5	12.0	896	14	US-10-176-847-98	Sequence 98, Appl

ALIGNMENTS

RESULT 1
US-09-888-077-1
; Sequence 1, Application US/09888077
; Patent No. US20020031818A1
; GENERAL INFORMATION:
; APPLICANT: Ronai, Ze'ev
; APPLICANT: Fuchs, Serge
; TITLE OF INVENTION: Modification of Mdm2 Activity
; FILE REFERENCE: 2420/1H195-US1
; CURRENT APPLICATION NUMBER: US/09/888,077
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,343
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-888-077-1

Query Match 100.0%; Score 553; DB 9; Length 491;
Best Local Similarity 100.0%; Pred. No. 1.3e-57;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125
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RESULT 2
US-09-956-425-8

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; Sequence 8, Application US/09956425
; Patent No. US20020045192A1
; GENERAL INFORMATION:
;  APPLICANT: Kriwacki, Richard
;  APPLICANT:  Bothner, Brian
;  APPLICANT:  Lewis, William
;  TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and Method of Use Thereof
;  FILE REFERENCE: 1340/1/035
;  CURRENT APPLICATION NUMBER: US/09/956,425
;  CURRENT FILING DATE:  2001-09-19
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-956-425-8

  Query Match             100.0%;  Score 553;  DB 9;  Length 491;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-57;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
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Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
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Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 3
US-09-029-327-2
; Sequence 2, Application US/09029327
; Publication No. US20030060432A1
;  GENERAL INFORMATION:
;    APPLICANT:  TOCQUE, Bruno
;    APPLICANT:  WASYLYK, Bohdan
;    APPLICANT:  DUBS-POTERSZMAN,
;    APPLICANT:  Marie-Christine
;    TITLE OF INVENTION:  ANTAGONISTS OF THE ONCOGENIC ACTIVITY OF
;    TITLE OF INVENTION:  THE PROTEIN MDM2, AND USE THEREOF IN THE TREATMENT OF
;    TITLE OF INVENTION:  CANCERS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rhone-Poulenc Rorer Inc.
;      STREET:  500 Arcola Road, Mailstop 3C43
;      CITY:  Collegeville
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19426
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/029,327
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR 96/01340
;      FILING DATE:  02-SEP-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO FR95/10331
;      FILING DATE:  04-SEP-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fehlner Esq., Paul F.
;      REGISTRATION NUMBER:  35,135
;      REFERENCE/DOCKET NUMBER:  ST95050-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (610) 454-3839
;      TELEFAX:  (610) 454-3808
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-029-327-2

  Query Match             100.0%;  Score 553;  DB 10;  Length 491;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-57;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
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RESULT 4
US-09-966-724-2
; Sequence 2, Application US/09966724
; Publication No. US20040170971A1
;  GENERAL INFORMATION:
;       APPLICANT: THE JOHNS HOPKINS UNIVERSITY
;                  720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA
;       TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
;                           HUMAN TUMORS
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
;            STREET: 1001 G ST., N.W.
;            CITY: WASHINGTON
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20001-4597
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/966,724
;            FILING DATE: 01-Oct-2001
;            CLASSIFICATION: 435
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/044,619
;            FILING DATE: 2001-10-01
;            APPLICATION NUMBER: US 07/867.840
;            FILING DATE: 07-APR-1992
;       ATTORNEY/AGENT INFORMATION:
;            NAME: KAGAN, SARAH A.
;            REGISTRATION NUMBER: 32,141
;            REFERENCE/DOCKET NUMBER: 01107.40148
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-508-9100
;            TELEFAX: 202-508-9299
;            TELEX: 197430 BBMB UT
;  INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 491 amino acids
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;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
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  Best Local Similarity   100.0%;  Pred. No. 1.3e-57;
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RESULT 5
US-10-422-536-137
; Sequence 137, Application US/10422536
; Publication No. US20040014100A1
; GENERAL INFORMATION:
;  APPLICANT: Kinsella, Todd
;  APPLICANT:  Lorens, James
;  APPLICANT:  Pray, Todd
;  APPLICANT:  Bennett, Mark
;  TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR INHIBITING
;  TITLE OF INVENTION:  PROTEIN-PROTEIN INTERACTION
;  FILE REFERENCE: A-71433-1/AMP/CYO
;  CURRENT APPLICATION NUMBER: US/10/422,536
;  CURRENT FILING DATE:  2003-04-23
;  PRIOR APPLICATION NUMBER: US 60/187,130
;  PRIOR FILING DATE: 2000-03-06
;  PRIOR APPLICATION NUMBER: US 09/800,770
;  PRIOR FILING DATE: 2001-03-06
;  PRIOR APPLICATION NUMBER: US 10/232,758
;  PRIOR FILING DATE: 2002-08-30
;  NUMBER OF SEQ ID NOS: 168
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 137
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-422-536-137

  Query Match            100.0%;  Score 553;  DB 15;  Length 491;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-57;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
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Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 6
US-10-232-951-35
; Sequence 35, Application US/10232951
; Publication No. US20040043386A1
; GENERAL INFORMATION:
;  APPLICANT: Pray, Todd
;  APPLICANT:  Wong, Brian
;  APPLICANT:  Bennett, Mark
;  APPLICANT:  Parlati, Francesco
;  APPLICANT:  Rigel Pharmaceuticals, Incorporated
;  TITLE OF INVENTION: Methods and Compositions for Functional Ubiquitin
;  TITLE OF INVENTION:  Assays
;  FILE REFERENCE: 021044-006800US
;  CURRENT APPLICATION NUMBER: US/10/232,951
;  CURRENT FILING DATE:  2002-08-30
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: E3 ubiquitin ligating agent mouse double minute 2
;   OTHER INFORMATION: (mdm2) homolog full length protein isoform, mouse
;   OTHER INFORMATION: p53-binding protein (MDM2) homolog, transcript
;   OTHER INFORMATION: variant MDM2, transformed 3T3 cell double minute 2,
;   OTHER INFORMATION: Mdm2 cDNA
US-10-232-951-35

  Query Match            100.0%;  Score 553;  DB 15;  Length 491;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-57;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 7
US-10-685-838-1
; Sequence 1, Application US/10685838
; Publication No. US20040197893A1
; GENERAL INFORMATION:
;  APPLICANT: SHUBERT, CARSTEN
;  APPLICANT:  GRASBERGER, BRUCE
;  APPLICANT:  MAGUIRE, DIANE
;  APPLICANT:  DECKMAN, INGRID
;  APPLICANT:  SPURLINO, JOHN
;  TITLE OF INVENTION: HDM2-INHIBITOR COMPLEXES AND USES THEREOF
;  FILE REFERENCE: PRD-2137-USANP
;  CURRENT APPLICATION NUMBER: US/10/685,838
;  CURRENT FILING DATE:  2003-10-15
;  PRIOR APPLICATION NUMBER: 60/418,350
;  PRIOR FILING DATE: 2002-10-16
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-685-838-1

  Query Match            100.0%;  Score 553;  DB 17;  Length 491;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-57;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 8
US-10-724-225-2
; Sequence 2, Application US/10724225
; Publication No. US20040209834A1
;  GENERAL INFORMATION:
;       APPLICANT: TOCQUE, Bruno
;                  WASYLYK, Bohdan
;                  DUBS-POTERSZMAN,
;                  Marie-Christine
;       TITLE OF INVENTION: ANTAGONISTS OF THE ONCOGENIC ACTIVITY OF
;                           THE PROTEIN MDM2, AND USE THEREOF IN THE TREATMENT OF
;                           CANCERS
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Rhone-Poulenc Rorer Inc.
;            STREET: 500 Arcola Road, Mailstop 3C43
;            CITY: Collegeville
```

```
;               STATE: PA
;               COUNTRY: USA
;               ZIP: 19426
;          COMPUTER READABLE FORM:
;               MEDIUM TYPE: Floppy disk
;               COMPUTER: IBM PC compatible
;               OPERATING SYSTEM: PC-DOS/MS-DOS
;               SOFTWARE: PatentIn Release #1.0, Version #1.30
;          CURRENT APPLICATION DATA:
;               APPLICATION NUMBER: US/10/724,225
;               FILING DATE: 01-Dec-2003
;               CLASSIFICATION: 514
;          PRIOR APPLICATION DATA:
;               APPLICATION NUMBER: US/09/029,327
;               FILING DATE: <Unknown>
;               APPLICATION NUMBER: FR 96/01340
;               FILING DATE: 02-SEP-1996
;               APPLICATION NUMBER: WO FR95/10331
;               FILING DATE: 04-SEP-1995
;          ATTORNEY/AGENT INFORMATION:
;               NAME: Fehlner Esq., Paul F.
;               REGISTRATION NUMBER: 35,135
;               REFERENCE/DOCKET NUMBER: ST95050-US
;          TELECOMMUNICATION INFORMATION:
;               TELEPHONE: (610) 454-3839
;               TELEFAX: (610) 454-3808
;     INFORMATION FOR SEQ ID NO: 2:
;          SEQUENCE CHARACTERISTICS:
;               LENGTH: 491 amino acids
;               TYPE: amino acid
;               TOPOLOGY: linear
;          MOLECULE TYPE: protein
;          SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-724-225-2

  Query Match             100.0%;  Score 553;  DB 17;  Length 491;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-57;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 9
US-10-489-802-8
; Sequence 8, Application US/10489802
; Publication No. US20040248198A1
; GENERAL INFORMATION:
;  APPLICANT: St. Jude Children's Research Hospital, Inc.
;  APPLICANT:  Kriwacki, Richard
;  APPLICANT:  Bothner, Brian
;  APPLICANT:  Lewis, William
;  TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and
;  TITLE OF INVENTION:  Method of Use Thereof
;  FILE REFERENCE: 44158/243642
;  CURRENT APPLICATION NUMBER: US/10/489,802
;  CURRENT FILING DATE:  2004-03-16
;  PRIOR APPLICATION NUMBER: US 09/956,425
;  PRIOR FILING DATE: 2001-09-19
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-489-802-8

  Query Match             100.0%;  Score 553;  DB 17;  Length 491;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-57;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 10
US-10-723-860-2236
; Sequence 2236, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
;  APPLICANT: Aziz, Natasha
;  APPLICANT:  Ginsburg, Wendy M.
;  APPLICANT:  Zlotnik, Albert
;  TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
;  TITLE OF INVENTION:  Methods for Screening for Soft Tissue Sarcoma Modulators
;  FILE REFERENCE: 05882.0193.NPUS01
;  CURRENT APPLICATION NUMBER: US/10/723,860
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: 60/429,739
;  PRIOR FILING DATE: 2002-11-26
;  NUMBER OF SEQ ID NOS: 8393
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2236
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-723-860-2236

  Query Match             100.0%;  Score 553;  DB 17;  Length 491;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-57;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 11
US-10-057-510-4
; Sequence 4, Application US/10057510
; Publication No. US20020098580A1
; GENERAL INFORMATION:
;  APPLICANT: Nandabalan, Krishnan
;  APPLICANT:  Yang, Meijia
;  APPLICANT:  Schulz, Vincent
;  APPLICANT:  CuraGen Corporation
;  TITLE OF INVENTION: MDM INTERACTING PROTEIN AND METHODS OF USE THEREOF
;  FILE REFERENCE: 15966-524 MDM US
;  CURRENT APPLICATION NUMBER: US/10/057,510
;  CURRENT FILING DATE:  2002-01-25
;  PRIOR APPLICATION NUMBER: USSN 09/510,252
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: USSN 60/121,192
;  PRIOR FILING DATE: 1999-02-23
;  PRIOR APPLICATION NUMBER: USSN 60/122,643
;  PRIOR FILING DATE: 1999-03-03
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 216
;   TYPE: PRT
;   ORGANISM: Homo sapiens
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US-10-057-510-4

Query Match 97.0%; Score 536.5; DB 13; Length 216;
Best Local Similarity 99.1%; Pred. No. 4.4e-56;
Matches 108; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYL-QYIMTKRLYDEKQQHIVY 75

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 124
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RESULT 12
US-10-287-226-380
; Sequence 380, Application US/10287226
; Publication No. US20040086875A1
; GENERAL INFORMATION:
; APPLICANT: Agee, Michele L.,
; APPLICANT: Alsobrook, John P.,
; APPLICANT: Berghs, Constance,
; APPLICANT: Boldog, Ference,
; APPLICANT: Burgess, Catherine E.,
; APPLICANT: Chant, John S.,
; APPLICANT: Chaudhuri, Amitabha,
; APPLICANT: DiPippo, Vincent A.,
; APPLICANT: Edinger, Shlomit R.,
; APPLICANT: Eisen, Andrew,
; APPLICANT: Ellerman, Karen,
; APPLICANT: Gangolli, Esha A.,
; APPLICANT: Gorman, Linda,
; APPLICANT: Gerlach, Valerie,
; APPLICANT: Ji, Weizhen,
; APPLICANT: Kekuda, Ramesh,
; APPLICANT: Khramtsov, Nikolai,
; APPLICANT: Li, Li,
; APPLICANT: Malyankar, Uriel M.,
; APPLICANT: MacDougall, John R.,
; APPLICANT: Mezes, Peter S.
; APPLICANT: Miller, Charles E.,
; APPLICANT: Millet, Isabelle,
; APPLICANT: Ooi, Chean Eng,
; APPLICANT: Ort, Tatiana,
; APPLICANT: Padigaru, Muralidhara,
; APPLICANT: Patturajan, Meera,
; APPLICANT: Rastelli, Luca,
; APPLICANT: Rieger, Daniel K.,
; APPLICANT: Rothenberg, Mark E.,
; APPLICANT: Shenoy, Suresh G.,
; APPLICANT: Spaderna, Steven K.,
; APPLICANT: Spytek, Kimberley A.,
; APPLICANT: Taupier, Jr., Raymond J.,
; APPLICANT: Vernet, Corine A.M.,
; APPLICANT: Zerhusen, Bryan D.,
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-480C
; CURRENT APPLICATION NUMBER: US/10/287,226
; CURRENT FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: 60/334,421
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/354,392
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/360,148
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 60/364,000
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/404,821
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 60/334,526
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/354,409
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/364,227
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/334,027
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/331,641
; PRIOR FILING DATE: 2001-11-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 673
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 380
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-226-380

Query Match 95.4%; Score 527.5; DB 15; Length 522;
Best Local Similarity 77.9%; Pred. No. 1.7e-54;
Matches 109; Conservative 0; Mismatches 0; Indels 31; Gaps 1;

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Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKE---------------------- 36
              ||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKERWSFTMLPRLVWNSWAQGICLPRP 76

Qy         37 -------VLFYLGQYIMTKRLYDEKQQHIVYCSNDLLGDLFGVPSFSVKEHRKIYTMIYR 89
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 PKVLDLQVLFYLGQYIMTKRLYDEKQQHIVYCSNDLLGDLFGVPSFSVKEHRKIYTMIYR 136

Qy         90 NLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||
Db        137 NLVVVNQQESSDSGTSVSEN 156
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RESULT 13
US-10-287-226-382
; Sequence 382, Application US/10287226
; Publication No. US20040086875A1
; GENERAL INFORMATION:
; APPLICANT: Agee, Michele L.,
; APPLICANT: Alsobrook, John P.,
; APPLICANT: Berghs, Constance,
; APPLICANT: Boldog, Ference,
; APPLICANT: Burgess, Catherine E.,
; APPLICANT: Chant, John S.,
; APPLICANT: Chaudhuri, Amitabha,
; APPLICANT: DiPippo, Vincent A.,
; APPLICANT: Edinger, Shlomit R.,
; APPLICANT: Eisen, Andrew,
; APPLICANT: Ellerman, Karen,
; APPLICANT: Gangolli, Esha A.,
; APPLICANT: Gorman, Linda,
; APPLICANT: Gerlach, Valerie,
; APPLICANT: Ji, Weizhen,
; APPLICANT: Kekuda, Ramesh,
; APPLICANT: Khramtsov, Nikolai,
; APPLICANT: Li, Li,
; APPLICANT: Malyankar, Uriel M.,
; APPLICANT: MacDougall, John R.,
; APPLICANT: Mezes, Peter S.
; APPLICANT: Miller, Charles E.,
; APPLICANT: Millet, Isabelle,
; APPLICANT: Ooi, Chean Eng,
; APPLICANT: Ort, Tatiana,
; APPLICANT: Padigaru, Muralidhara,
; APPLICANT: Patturajan, Meera,
; APPLICANT: Rastelli, Luca,
; APPLICANT: Rieger, Daniel K.,
; APPLICANT: Rothenberg, Mark E.,
; APPLICANT: Shenoy, Suresh G.,
; APPLICANT: Spaderna, Steven K.,
; APPLICANT: Spytek, Kimberley A.,
; APPLICANT: Taupier, Jr., Raymond J.,

```
;  APPLICANT:  Vernet, Corine A.M.,
;  APPLICANT:  Zerhusen, Bryan D.,
;  APPLICANT:  Zhong, Mei
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-480C
;  CURRENT APPLICATION NUMBER: US/10/287,226
;  CURRENT FILING DATE:  2002-11-04
;  PRIOR APPLICATION NUMBER: 60/334,421
;  PRIOR FILING DATE: 2001-11-30
;  PRIOR APPLICATION NUMBER: 60/354,392
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: 60/360,148
;  PRIOR FILING DATE: 2002-02-27
;  PRIOR APPLICATION NUMBER: 60/364,000
;  PRIOR FILING DATE: 2002-03-13
;  PRIOR APPLICATION NUMBER: 60/404,821
;  PRIOR FILING DATE: 2002-08-20
;  PRIOR APPLICATION NUMBER: 60/334,526
;  PRIOR FILING DATE: 2001-11-30
;  PRIOR APPLICATION NUMBER: 60/354,409
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: 60/364,227
;  PRIOR FILING DATE: 2002-03-13
;  PRIOR APPLICATION NUMBER: 60/334,027
;  PRIOR FILING DATE: 2001-11-28
;  PRIOR APPLICATION NUMBER: 60/331,641
;  PRIOR FILING DATE: 2001-11-20
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 673
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 382
;   LENGTH: 522
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-287-226-382

  Query Match             95.4%;  Score 527.5;  DB 15;  Length 522;
  Best Local Similarity   77.9%;  Pred. No. 1.7e-54;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels   31;  Gaps    1;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKE----------------------- 36
              ||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKERWSFTMLPRLVWNSWAQGICLPRP 76

Qy         37 -------VLFYLGQYIMTKRLYDEKQQHIVYCSNDLLGDLFGVPSFSVKEHRKIYTMIYR 89
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 PKVLDLQVLFYLGQYIMTKRLYDEKQQHIVYCSNDLLGDLFGVPSFSVKEHRKIYTMIYR 136

Qy         90 NLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||
Db        137 NLVVVNQQESSDSGTSVSEN 156


RESULT 14
US-09-956-425-6
; Sequence 6, Application US/09956425
; Patent No. US20020045192A1
; GENERAL INFORMATION:
;  APPLICANT: Kriwacki, Richard
;  APPLICANT:  Bothner, Brian
;  APPLICANT:  Lewis, William
;  TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and Method of Use Thereof
;  FILE REFERENCE: 1340/1/035
;  CURRENT APPLICATION NUMBER: US/09/956,425
;  CURRENT FILING DATE:  2001-09-19
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 489
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-956-425-6

  Query Match             89.2%;  Score 493.5;  DB 9;  Length 489;
  Best Local Similarity   88.1%;  Pred. No. 2e-50;
  Matches   96;  Conservative    7;  Mismatches    3;  Indels    3;  Gaps    1;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              |||||||||||||||||||||||||||| ||||||::||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQNDTYTMKEIIFYIGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||:|||||||||||||| |||||| |:||   |||||:||:
Db         77 CSNDLLGDVFGVPSFSVKEHRKIYAMIYRNLVAVSQQ---DSGTSLSES 122


RESULT 15
US-09-966-724-4
; Sequence 4, Application US/09966724
; Publication No. US20040170971A1
;  GENERAL INFORMATION:
;       APPLICANT: THE JOHNS HOPKINS UNIVERSITY
;                  720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA
;       TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
;                           HUMAN TUMORS
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
;            STREET: 1001 G ST., N.W.
;            CITY: WASHINGTON
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20001-4597
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/966,724
;            FILING DATE: 01-Oct-2001
;            CLASSIFICATION: 435
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/044,619
;            FILING DATE: 2001-10-01
;            APPLICATION NUMBER: US 07/867.840
;            FILING DATE: 07-APR-1992
;       ATTORNEY/AGENT INFORMATION:
;            NAME: KAGAN, SARAH A.
;            REGISTRATION NUMBER: 32,141
;            REFERENCE/DOCKET NUMBER: 01107.40148
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-508-9100
;            TELEFAX: 202-508-9299
;            TELEX: 197430 BBMB UT
;   INFORMATION FOR SEQ ID NO: 4:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 489 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-966-724-4

  Query Match             89.2%;  Score 493.5;  DB 11;  Length 489;
  Best Local Similarity   88.1%;  Pred. No. 2e-50;
  Matches   96;  Conservative    7;  Mismatches    3;  Indels    3;  Gaps    1;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 60
              |||||||||||||||||||||||||||| ||||||::||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQNDTYTMKEIIFYIGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||:|||||||||||||| |||||| |:||   |||||:||:
Db         77 CSNDLLGDVFGVPSFSVKEHRKIYAMIYRNLVAVSQQ---DSGTSLSES 122
```

Search completed: January 27, 2005, 18:23:04
Job time : 75.4 secs

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:45:30 ; Search time 80.8 Seconds
(without alignments)
483.929 Million cell updates/sec

Title: US-10-822-254-4
Perfect score: 521
Sequence: 1 SQIPASEQETXVRPKPXLLK.....NLVVVNQQESSDSGTSVSEN 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	506	97.1	284	2	AAR75494	Aar75494 Human dou
2	506	97.1	284	2	AAR75397	Aar75397 Human dou
3	506	97.1	491	2	AAR42175	Aar42175 Human MDM
4	506	97.1	491	2	AAR76696	Aar76696 Human MDM
5	506	97.1	491	2	AAW07887	Aaw07887 Human MDM
6	506	97.1	491	2	AAW15463	Aaw15463 Human MDM
7	506	97.1	491	2	AAW13380	Aaw13380 Human MDM
8	506	97.1	491	2	AAW13600	Aaw13600 Murine do
9	506	97.1	491	2	AAW48241	Aaw48241 Human MDM
10	506	97.1	491	2	AAW57241	Aaw57241 Human MDM
11	506	97.1	491	2	AAW42879	Aaw42879 Amino aci
12	506	97.1	491	2	AAW42971	Aaw42971 Amino aci
13	506	97.1	491	2	AAW94304	Aaw94304 Human MDM
14	506	97.1	491	3	AAY96567	Aay96567 MDM2 onco
15	506	97.1	491	4	AAB48284	Aab48284 Human MDM
16	506	97.1	491	5	AAE22654	Aae22654 Human Rin
17	506	97.1	491	5	AAE22698	Aae22698 Human Rin
18	506	97.1	491	5	AAE25913	Aae25913 Human dou
19	506	97.1	491	5	AAO15376	Aao15376 Human Dm2
20	506	97.1	491	7	ADD21815	Add21815 Human mdm
21	506	97.1	491	7	ADE61562	Ade61562 Human Pro
22	506	97.1	491	8	ADL23893	Adl23893 Human E3
23	506	97.1	491	8	ADO52353	Ado52353 Human p53
24	506	97.1	491	8	ADP12593	Adp12593 Protein e
25	506	97.1	491	8	ADN71936	Adn71936 MDM2 prot
26	506	97.1	491	8	ADQ19417	Adq19417 Human sof
27	506	97.1	1171	4	AAU32421	Aau32421 Novel hum
28	489.5	94.0	216	3	AAB08846	Aab08846 A human M
29	480.5	92.2	522	7	ADJ95152	Adj95152 Novel NOV
30	480.5	92.2	522	7	ADJ95154	Adj95154 Novel NOV
31	446.5	85.7	489	2	AAR42176	Aar42176 Murine MD
32	446.5	85.7	489	2	AAR76697	Aar76697 Mouse MDM
33	446.5	85.7	489	2	AAW07888	Aaw07888 Murine MD
34	446.5	85.7	489	2	AAW15464	Aaw15464 Murine MD
35	446.5	85.7	489	2	AAW48242	Aaw48242 Mouse MDM
36	446.5	85.7	489	2	AAW57246	Aaw57246 Mouse MDM
37	446.5	85.7	489	2	AAW42997	Aaw42997 Amino aci
38	446.5	85.7	489	2	AAW42972	Aaw42972 Amino aci
39	446.5	85.7	489	2	AAW94305	Aaw94305 Mouse MDM
40	446.5	85.7	489	5	AAE25914	Aae25914 Mouse dou
41	446.5	85.7	489	5	ABB57099	Abb57099 Mouse isc
42	446.5	85.7	489	5	AAO15375	Aao15375 Mouse Dm2
43	446.5	85.7	489	7	ADD21816	Add21816 Mouse mdm
44	446.5	85.7	489	7	ADE61560	Ade61560 Rat Prote
45	322	61.8	227	2	AAR75495	Aar75495 Human dou

ALIGNMENTS

RESULT 1
AAR75494
ID AAR75494 standard; protein; 284 AA.
XX
AC AAR75494;
XX
DT 02-FEB-1996 (first entry)
XX
DE Human double minute 2 (hdm-2) antibody-binding region fragment 1.
XX
KW Human double minute gene 2; hdm-2; antibody binding region; antigen;
KW cancer; sarcoma; rhabdomyosarcoma; diagnosis; immunoassay.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1. .284
FT /note= "amino acids 1-284 of hdm-2 gene product"
XX
PN DE4339533-A1.
XX
PD 14-JUN-1995.
XX
PF 19-NOV-1993; 93DE-04339533.
XX
PR 19-NOV-1993; 93DE-04339533.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Zentgraf H, Klein R, Frey M, Martens R;
XX
DR WPI; 1995-216248/29.
DR N-PSDB; AAQ92515.
XX
PT Detection of human double minute gene 2 (hdm-2) antibodies - by
PT incubation with new hdm-2 or antibody-binding hdm-2 fragments; useful in
PT the detection of specific cancers.
XX
PS Claim 11; Fig 1; 12pp; German.
XX
CC Fragments contg. amino acids 1-284, 58-284 and 58-491 of the hdm-2 (human
CC double minute 2) gene product are claimed. The overlapping protein
CC fragments contain binding regions for hdm-2- specific antibodies and are
CC useful for identifying such antibodies in a claimed immunoassay method.
CC The presence of anti-hdm-2 antibodies is diagnostic of certain forms of
CC cancer, e.g. rhabdomyosarcoma
XX
SQ Sequence 284 AA;

```
  Query Match             97.1%;  Score 506;  DB 2;  Length 284;
  Best Local Similarity   93.6%;  Pred. No. 1e-59;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||| ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 2
AAR75397
ID   AAR75397 standard; protein; 284 AA.
XX
AC   AAR75397;
XX
DT   25-MAR-2003  (revised)
DT   25-JAN-1996  (first entry)
XX
DE   Human double minute 2 (hdm-2) antibody-binding region fragment 1.
XX
KW   Human double minute gene 2; hdm-2; antibody binding region; antigen;
KW   cancer; sarcoma; rhabdomyosarcoma; diagnosis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .284
FT                   /note= "amino acids 1-284 of hdm-2 gene product"
XX
PN   DE4345249-A1.
XX
PD   24-MAY-1995.
XX
PF   19-NOV-1993;   93DE-04345249.
XX
PR   19-NOV-1993;   93DE-04339533.
XX
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI   Zentgraf H,  Klein R,  Frey M,  Martens R;
XX
DR   WPI; 1995-195167/26.
DR   N-PSDB; AAQ87261.
XX
PT   New hdm-2 fragments contg. antibody binding region - used to detect
PT   specific antibodies for diagnosis of cancers, also new DNA sequences
PT   encoding them.
XX
PS   Claim 2; Fig 1; 11pp; German.
XX
CC   Fragments contg. amino acids 1-284, 58-284 and 58-491 of the hdm-2 (human
CC   double minute 2) gene product are claimed. The overlapping protein
CC   fragments contain binding regions for hdm-2- specific antibodies and are
CC   useful for identifying such antibodies. The presence of anti-hdm-2
CC   antibodies is diagnostic of certain forms of cancer, e.g.
CC   rhabdomyosarcoma. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 284 AA;

  Query Match             97.1%;  Score 506;  DB 2;  Length 284;
  Best Local Similarity   93.6%;  Pred. No. 1e-59;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||| ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 3
AAR42175
ID   AAR42175 standard; protein; 491 AA.
XX
AC   AAR42175;
XX
DT   25-MAR-2003  (revised)
DT   05-MAY-1994  (first entry)
XX
DE   Human MDM2.
XX
KW   p53 gene; tumour suppressor gene; regulation; cellular proliferation;
KW   cellular transformation; carcinoma; human; tumour; MDM2; inhibition;
KW   gene amplification.
XX
OS   Homo sapiens.
XX
PN   WO9320238-A2.
XX
PD   14-OCT-1993.
XX
PF   07-APR-1993;   93WO-US003199.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Burrell M,  Hill DE,  Kinzler KW,  Vogelstein B;
XX
DR   WPI; 1993-336944/42.
DR   N-PSDB; AAQ49891.
XX
PT   Diagnosing neoplasia from amplification of MDM2 gene - or elevated gene
PT   expression, also new DNA, MDM2 protein, antibodies and treatment of
PT   sarcoma by inhibiting MDM2 expression.
XX
PS   Claim 19; Fig 1; 75pp; English.
XX
CC   This sequence is encoded by the MDM2 gene. Amplification of the MDM2 gene
CC   is diagnostic of neoplasia or the potential for neoplasia. The protein
CC   encoded by this gene interacts with the product of the p53 gene. p53 is a
CC   tumour suppressor gene and encodes a protein which appears to be a member
CC   of a group of proteins which regulate normal cellular proliferation and
CC   suppression of cellular transformation. Inactivation of the p53 gene has
CC   been implicated in the formation, or progression of a wide variety of
CC   carcinoma. Polypeptides containing at least amino acids 13-41 of p53, or
CC   the DNA encoding these, may be used to inhibit the growth of tumour cells
CC   containing MDM2 gene amplification. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 491 AA;

  Query Match             97.1%;  Score 506;  DB 2;  Length 491;
  Best Local Similarity   93.6%;  Pred. No. 2.2e-59;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||| ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 4
AAR76696
ID   AAR76696 standard; protein; 491 AA.
```

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XX
AC   AAR76696;
XX
DT   16-OCT-2003  (revised)
DT   01-NOV-1995  (first entry)
XX
DE   Human MDM2 protein.
XX
KW   MDM2; sarcoma; diagnostic; DNA probe.
XX
OS   Homo sapiens; (cell line CaCo-2).
XX
PN   US5420263-A.
XX
PD   30-MAY-1995.
XX
PF   07-APR-1993;   93US-00044619.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Vogelstein B,  Kinzler KW;
XX
DR   WPI; 1995-206312/27.
DR   N-PSDB; AAQ94589.
XX
PT   New human MDM2 cDNA - used to develop prods. for use in the diagnosis and
PT   treatment of tumours.
XX
PS   Claim 1; Col 23-26; 34pp; English.
XX
CC   The human MDM2 gene is genetically altered (i.e. amplified) in human
CC   tumour cells. The human MDM2 protein binds to human p53 and allows the
CC   cell to escape from p53-regulated growth. Detecting that the gene has
CC   become amplified or detecting increased gene product expression (using
CC   probes, proteins, antibodies and inhibitors) allows diagnosis and therapy
CC   of cancers such as colorectal carcinoma, lung cancer and chronic
CC   myelogenous leukaemia. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ   Sequence 491 AA;

  Query Match             97.1%;  Score 506;  DB 2;  Length 491;
  Best Local Similarity   93.6%;  Pred. No. 2.2e-59;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              ||||||||||*|||||*||||||||||||||||||*||||||||||||||||||||||*
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              ||||*|||||||*|||||||||||||||*||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 5
AAW07887
ID   AAW07887 standard; protein; 491 AA.
XX
AC   AAW07887;
XX
DT   25-MAR-2003  (revised)
DT   28-JAN-1997  (first entry)
XX
DE   Human MDM-2, involved in tumour-development.
XX
KW   p53; MDM-2; binding-inhibitor; identification; tumour; cancer; neoplasia;
KW   antibody fusion protein; therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   166. .169
FT                   /label= phosphorylation_site
FT                   /note= "potential casein kinase II phosphorylation site"
FT   Binding-site    181. .185
FT                   /label= nuclear_localisation_signal
FT   Modified-site   192. .195
FT                   /label= phosphorylation_site
FT                   /note= "potential casein kinase II phosphorylation site"
FT   Domain          223. .274
FT                   /label= acid_activation_domain
FT   Modified-site   269. .272
FT                   /label= phosphorylation_site
FT                   /note= "potential casein kinase II phosphorylation site"
FT   Modified-site   290. .293
FT                   /label= phosphorylation_site
FT                   /note= "potential casein kinase II phosphorylation site"
FT   Domain          305. .322
FT                   /label= metal_binding_site
FT   Domain          461. .478
FT                   /label= metal_binding_site
XX
PN   US5550023-A.
XX
PD   27-AUG-1996.
XX
PF   18-MAY-1994;   94US-00245500.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
PR   07-APR-1993;   93US-00044619.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Vogelstein B,  Kinzler KW;
XX
DR   WPI; 1996-401591/40.
DR   N-PSDB; AAT45151.
XX
PT   Identification of cpds. interfering with human MDM2/p53 binding - useful
PT   as therapeutic agents to treat human neoplastic cells.
XX
PS   Claim 26; Col 25-28; 36pp; English.
XX
CC   AAW07887 represents human MDM-2 derived from a human colon carcinoma cell
CC   line, CaCo-2, cDNA library. The MDM-2 protein is used in a method for
CC   identifying compounds that interfere with the binding of p53 and MDM-2.
CC   In binding the p53 protein, the MDM-2 protein releases a cell from p53-
CC   regulated growth, allowing cancers to develop. Therefore compounds
CC   identified as interfering with the binding of MDM-2 to p53 are
CC   potentially useful in the treatment of human neoplastic cells. In the
CC   method pref. one or both of the proteins is a fusion protein esp. with an
CC   antibody or antibody fragment which aids separation and identification.
CC   (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 491 AA;

  Query Match             97.1%;  Score 506;  DB 2;  Length 491;
  Best Local Similarity   93.6%;  Pred. No. 2.2e-59;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              ||||||||||*|||||*||||||||||||||||||*||||||||||||||||||||||*
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              ||||*|||||||*|||||||||||||||*||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 6
AAW15463
ID   AAW15463 standard; protein; 491 AA.
XX
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AC   AAW15463;
XX
DT   25-MAR-2003  (revised)
DT   18-JUN-1997  (first entry)
XX
DE   Human MDM2.
XX
KW   Human; MDM2 protein; antibody; detection; cancer; diagnosis;
KW   p53-regulated growth.
XX
OS   Homo sapiens.
XX
PN   US5618921-A.
XX
PD   08-APR-1997.
XX
PF   17-FEB-1995;   95US-00390479.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
PR   07-APR-1993;   93US-00044619.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Vogelstein B,  Kinzler KW,  Burrell M,  Hill DE;
XX
DR   WPI; 1997-225474/20.
DR   N-PSDB; AAT66410.
XX
PT   Antibodies specific for human MDM2 protein - for diagnosis of cancer.
XX
PS   Claim 1; Col 19-24; 35pp; English.
XX
CC   This sequence represents the human MDM2 protein. Antibodies that
CC   specifically bind to human MDM2 protein may be used for detecting
CC   elevated expression of the MDM2 gene in a human tissue or body fluid
CC   sample, esp. for cancer diagnosis. The antibodies may be used to
CC   interfere with the binding of p53 to MDM2. Elevated levels of MDM2 appear
CC   to sequester p53 and allow the cell to escape from p53-regulated growth.
CC   (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 491 AA;

  Query Match             97.1%;  Score 506;  DB 2;  Length 491;
  Best Local Similarity   93.6%;  Pred. No. 2.2e-59;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||| ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 7
AAW13380
ID   AAW13380 standard; protein; 491 AA.
XX
AC   AAW13380;
XX
DT   25-MAR-2003  (revised)
DT   05-JUN-1997  (first entry)
XX
DE   Human MDM2 protein.
XX
KW   Human; MDM2; CaCo-2; colonic; carcinoma; probe; detection; amplification;
KW   elevation; expression; diagnosis; neoplasia; neoplastic transformation;
KW   sarcoma; colorectal; lung cancer; chronic myelogenous leukaemia.
XX
OS   Homo sapiens.
XX
PN   US5606044-A.
XX
PD   25-FEB-1997.
XX
PF   17-FEB-1995;   95US-00390546.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
PR   07-APR-1993;   93US-00044619.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Kinzler KW,  Vogelstein B,  Hill DE,  Burrell M;
XX
DR   WPI; 1997-153623/14.
DR   N-PSDB; AAT62065.
XX
PT   Detection of amplification of human MDM2 gene - useful for diagnosis of
PT   neoplasia or potential neoplastic transformation.
XX
PS   Example 1; Col 21-24; 35pp; English.
XX
CC   The present sequence is the human MDM2 protein, the cDNA for which was
CC   isolated from a human CaCo-2 colonic carcinoma cell cDNA library using a
CC   murine MDM2 cDNA probe. The MDM2 cDNA can be used as a probe to detect
CC   the amplification or elevated expression of a human MDM2 gene, which is
CC   diagnostic of neoplasia or the potential for neoplastic transformation,
CC   useful for the detection of, e.g. sarcomas, colorectal carcinoma, lung
CC   cancer and chronic myelogenous leukaemia. (Updated on 25-MAR-2003 to
CC   correct PF field.)
XX
SQ   Sequence 491 AA;

  Query Match             97.1%;  Score 506;  DB 2;  Length 491;
  Best Local Similarity   93.6%;  Pred. No. 2.2e-59;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||| ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 8
AAW13600
ID   AAW13600 standard; protein; 491 AA.
XX
AC   AAW13600;
XX
DT   16-JAN-1998  (first entry)
XX
DE   Murine double minute 2 protein sequence.
XX
KW   Mouse; Mdm2; murine double minute; phosphoprotein; binding; modulation;
KW   tumour suppressor; p53; oncogene; cell cycle arrest; p107; antagonist;
KW   inhibition; transcription factor; adenocarcinoma; colon; cancer; breast;
KW   lung; stomach; myeloid leukaemia; lymphoma; hyperproliferative;
KW   restenosis.
XX
OS   Mus musculus.
XX
PN   WO9709343-A2.
XX
PD   13-MAR-1997.
XX
PF   02-SEP-1996;   96WO-FR001340.
XX
PR   04-SEP-1995;   95FR-00010331.
XX
PA   (RHON ) RHONE POULENC RORER SA.
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PA   (INRM ) INST NAT SANTE & RECH MEDICALE.
XX
PI   Tocque B,  Dubs-Poterszman M,  Wasylyk B;
XX
DR   WPI; 1997-192837/17.
DR   N-PSDB; AAT61637.
XX
PT   Treating cancer with antagonist of oncogenic activity of protein Mdm2 -
PT   or nucleic acid encoding an antagonist, also viral vectors contg. this
PT   nucleic acid.
XX
PS   Claim 2; Page 26-30; 43pp; French.
XX
CC   This is the amino acid sequence of the mouse Mdm2 (murine double minute-
CC   2) protein, a 90 kD phosphoprotein which binds and modulates the activity
CC   of the tumour suppressor protein p53. It has now been shown that the mdm2
CC   protein itself has oncogenic properties, especially in a p53-null
CC   background. Mdm2 is observed to unblock cell cycle arrest in G1 caused by
CC   over-expression of the p107 protein. This is especially done by the
CC   region covering amino acid 1-134. The invention therefore relates to
CC   antagonists able to inhibit the oncogenic activity of mdm2. These include
CC   fragments of the p53 protein, especially amino acids 1-52, 1-41, 6-41, 16
CC   -25 or 18-23 (AAW13602-6), or fragments of transcription factors e.g.
CC   TFII, TBP or TAF250, which bind amino acids 1-134 of mdm2. Other
CC   inhibitors include compounds which disrupt binding to region 135-491 of
CC   mdm2, e.g. Rb, L5 or the transcription factor E2F. The antagonists are
CC   used to treat e.g. adenocarcinoma of the colon; cancer of the breast,
CC   lung or stomach; myeloid leukaemia; B cell lymphoma, or other
CC   hyperproliferative conditions such as restenosis
XX
SQ   Sequence 491 AA;

  Query Match             97.1%;  Score 506;  DB 2;  Length 491;
  Best Local Similarity   93.6%;  Pred. No. 2.2e-59;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| ||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||||| ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 9
AAW48241
ID   AAW48241 standard; protein; 491 AA.
XX
AC   AAW48241;
XX
DT   18-JUN-1998  (first entry)
XX
DE   Human MDM2.
XX
KW   Human; MDM2; hMDM2; tumour; cancer; diagnosis; neoplastic disease;
KW   sarcoma; liposarcoma; malignant fibrous histiocytoma; osteosarcoma.
XX
OS   Homo sapiens.
XX
PN   US5736338-A.
XX
PD   07-APR-1998.
XX
PF   17-FEB-1995;   95US-00390517.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
PR   07-APR-1993;   93US-00044619.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Vogelstein B,  Kinzler KW,  Hill DE,  Burrell M;
XX
DR   WPI; 1998-239206/21.
DR   N-PSDB; AAV20549.
XX
PT   Cancer diagnosis - by determination of MDM2 protein.
XX
PS   Claim 1; Col 25-28; 35pp; English.
XX
CC   The present sequence represents human MDM2 (hMDM2) which is used in the
CC   method of the present invention. The present invention describes a method
CC   for diagnosing a neoplastic disease caused by overexpression of MDM2
CC   protein. The method comprises detecting an elevated cellular amount of
CC   this protein. The method is useful for the diagnosis of sarcoma,
CC   especially liposarcoma, malignant fibrous histiocytoma or osteosarcoma
XX
SQ   Sequence 491 AA;

  Query Match             97.1%;  Score 506;  DB 2;  Length 491;
  Best Local Similarity   93.6%;  Pred. No. 2.2e-59;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| ||||||||||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||||| ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 10
AAW57241
ID   AAW57241 standard; protein; 491 AA.
XX
AC   AAW57241;
XX
DT   10-AUG-1998  (first entry)
XX
DE   Human MDM2 protein.
XX
KW   Human; p53; MDM2; tumour; growth inhibition; amplification;
KW   malignant fibrous histiocytoma; liposarcoma.
XX
OS   Homo sapiens.
XX
PN   US5756455-A.
XX
PD   26-MAY-1998.
XX
PF   17-FEB-1995;   95US-00390515.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
PR   07-APR-1993;   93US-00044619.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Vogelstein B,  Kinzler KW;
XX
DR   WPI; 1998-321574/28.
DR   N-PSDB; AAV28876.
XX
PT   Inhibiting growth of tumour cells having MDM2 gene amplification - with
PT   p53 protein fragment.
XX
PS   Claim 1; Col 23-28; 40pp; English.
XX
CC   A method has been developed for inhibiting the growth of tumour cells
CC   containing a human MDM2 gene amplification. The method comprises treating
CC   the tumour cells with a DNA molecule that expresses a polypeptide capable
CC   of binding to human MDM2 protein. The present sequence represents human
CC   MDM2 protein. The present invention describes three preferred
CC   polypeptides for binding human MDM2: (1) the polypeptide comprises amino
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CC   acids 1-50 of p53 (see AAW57240); (2) the polypeptide comprises amino
CC   acids 13-41 of p53 (see AAW57240) and at least none additional p53
CC   residues on the N- or C-terminal side, provided that the polypeptide
CC   lacks the homooligomerisation domain of p53; (3) the polypeptide
CC   comprises amino acids 13-41 of p53 (see AAW57241) and at least nine
CC   additional p53 residues on the N- or C-terminal side, provided that the
CC   polypeptide lacks amino acids 138-393 of p53. Some malignant fibrous
CC   histiocytomas and liposarcomas have an MDM2 gene amplification, so
CC   detection of increased expression of MDM2 gene products indicates
CC   tumourigenesis
XX
SQ   Sequence 491 AA;

  Query Match             97.1%;  Score 506;  DB 2;  Length 491;
  Best Local Similarity   93.6%;  Pred. No. 2.2e-59;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||| ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 11
AAW42879
ID   AAW42879 standard; protein; 491 AA.
XX
AC   AAW42879;
XX
DT   30-APR-1998  (first entry)
XX
DE   Amino acid sequence of human MDM2.
XX
KW   MDM2; tumour; diagnosis; neoplasia; DNA binding protein; p53 polypeptide;
KW   binding; tumour cell; p53-regulated growth; inhibition;
KW   anti-cancer agent.
XX
OS   Homo sapiens.
XX
PN   US5708136-A.
XX
PD   13-JAN-1998.
XX
PF   17-FEB-1995;   95US-00390516.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
PR   07-APR-1993;   93US-00044619.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Vogelstein B,  Kinzler KW,  Burrell M,  Hill DE;
XX
DR   WPI; 1998-100408/09.
XX
PT   Human MDM2 binding polypeptide - comprises fragments of p53, useful in re
PT   -establishing p53-regulated growth control in cells over-expressing MDM2.
XX
PS   Disclosure; Col 23-28; 41pp; English.
XX
CC   The present sequence represents human MDM2. The MDM2 gene is amplified in
CC   some human tumours. The amplification of this gene is diagnostic of
CC   neoplasia or its potential. It is speculated that the MDM2 protein is a
CC   potential DNA binding protein that functions in the modulation of
CC   expression of other genes and, when present in excess, inteferes with
CC   normal constraints on cell growth. A cell containing three recombinant
CC   DNA constructs was produced. These constructs encode an MDM2 protein
CC   fused to a sequence-specific DNA binding domain, a p53 polypeptide fused
CC   to a transcriptional activation domain, and a reporter gene downstream
CC   from a DNA element which is recognised by the sequence-specific DNA-
CC   binding domain. The cell is used to identify a compound which interferes
CC   with the binding of MDM2 and p53. Since MDM2 is overexpressed in tumour
CC   cells and since binding of MDM2 to p53 appears to allow tumour cells to
CC   escape from p53-regulated growth, compounds that inhibit such binding
CC   would be useful as anti-cancer agents
XX
SQ   Sequence 491 AA;

  Query Match             97.1%;  Score 506;  DB 2;  Length 491;
  Best Local Similarity   93.6%;  Pred. No. 2.2e-59;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||| ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 12
AAW42971
ID   AAW42971 standard; protein; 491 AA.
XX
AC   AAW42971;
XX
DT   29-APR-1998  (first entry)
XX
DE   Amino acid sequence of human MDM2.
XX
KW   MDM2; tumour; diagnosis; neoplasia; DNA binding protein; p53 polypeptide;
KW   binding; tumour cell; p53-regulated growth; inhibition;
KW   anti-cancer agent.
XX
OS   Homo sapiens.
XX
PN   US5702903-A.
XX
PD   30-DEC-1997.
XX
PF   13-NOV-1995;   95US-00557393.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
PR   07-APR-1993;   93US-00044619.
PR   18-MAY-1994;   94US-00245500.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Vogelstein B,  Kinzler KW;
XX
DR   WPI; 1998-076411/07.
DR   N-PSDB; AAV03607.
XX
PT   Cell containing reporter construct containing human MDM2 and p53 genes -
PT   for identifying compounds that interfere with binding of human MDM2 to
PT   human p53, useful as anti-cancer agents.
XX
PS   Disclosure; Coulmns 22-28; 37pp; English.
XX
CC   The present sequence represents human MDM2. The MDM2 gene is amplified in
CC   some human tumours. The amplification of this gene is diagnostic of
CC   neoplasia or its potential. It is speculated that the MDM2 protein is a
CC   potential DNA binding protein that functions in the modulation of
CC   expression of other genes and, when present in excess, inteferes with
CC   normal constraints on cell growth. A cell containing three recombinant
CC   DNA constructs was produced. These constructs encode an MDM2 protein
CC   fused to a sequence-specific DNA binding domain, a p53 polypeptide fused
CC   to a transcriptional activation domain, and a reporter gene downstream
CC   from a DNA element which is recognised by the sequence-specific DNA-
CC   binding domain. The cell is used to identify a compound which interferes
CC   with the binding of MDM2 and p53. Since MDM2 is overexpressed in tumour
```

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CC   cells and since binding of MDM2 to p53 appears to allow tumour cells to
CC   escape from p53-regulated growth, compounds that inhibit such binding
CC   would be useful as anti-cancer agents
XX
SQ   Sequence 491 AA;

  Query Match             97.1%;  Score 506;  DB 2;  Length 491;
  Best Local Similarity   93.6%;  Pred. No. 2.2e-59;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||| ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 13
AAW94304
ID   AAW94304 standard; protein; 491 AA.
XX
AC   AAW94304;
XX
DT   13-APR-1999  (first entry)
XX
DE   Human MDM2.
XX
KW   Human; MDM2; p53; tumourigenesis; growth regulation; diagnosis;
KW   malignant fibrous histocytoma; MFH; liposarcoma.
XX
OS   Homo sapiens.
XX
PN   US5858976-A.
XX
PD   12-JAN-1999.
XX
PF   14-FEB-1997;   97US-00801718.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
PR   07-APR-1993;   93US-00044619.
PR   17-FEB-1995;   95US-00390515.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Kinzler KW,  Vogelstein B;
XX
DR   WPI; 1999-152105/13.
DR   N-PSDB; AAX03947.
XX
PT   Inhibiting growth of tumour cells having MDM2 gene amplification - with
PT   MDM2-binding p53 fragment.
XX
PS   Claim 1; Col 23-28; 41pp; English.
XX
CC   The present invention describes: (1) a method for inhibiting the growth
CC   of tumour cells which contain a human MDM2 gene amplification, comprising
CC   administering to the cells a DNA molecule that expresses a polypeptide
CC   consisting of a portion of p53 i.e. amino acids 13-41 of the 64 amino
CC   acid sequence given in AAW94303, the polypeptide being capable of binding
CC   to human MDM2 (the present sequence); (2) a method as in (1) where the
CC   polypeptide lacks the homo-oligomerisation domain of p53; and (3) a
CC   method as in (1) where the polypeptide lacks amino acids 138-393 of p53.
CC   The method is useful for treating the following tumour types which have a
CC   MDM2 gene amplification: M-7 malignant fibrous histocytoma (MFH), M-20
CC   MFH, L-9 liposarcoma, KL7 liposarcoma, KL28 liposarcoma, KL30
CC   liposarcoma, and OSA-CL MFH
XX
SQ   Sequence 491 AA;

  Query Match             97.1%;  Score 506;  DB 2;  Length 491;
  Best Local Similarity   93.6%;  Pred. No. 2.2e-59;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||| ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 14
AAY96567
ID   AAY96567 standard; protein; 491 AA.
XX
AC   AAY96567;
XX
DT   12-SEP-2000  (first entry)
XX
DE   MDM2 oncoprotein.
XX
KW   hEST2; telomerase; catalytic subunit; reverse transcriptase; life-span;
KW   retinoblastoma; p53; tumour suppressor; inhibitor; arteriosclerosis;
KW   proliferation; immortal; tumour therapy; macular degeneration; activator;
KW   INK4; MDM2; oncoprotein.
XX
OS   Homo sapiens.
XX
PN   WO200031238-A2.
XX
PD   02-JUN-2000.
XX
PF   24-NOV-1999;   99WO-US027907.
XX
PR   25-NOV-1998;   98US-0109891P.
PR   17-FEB-1999;   99US-0120549P.
XX
PA   (GENE-) GENETICA INC.
XX
PI   Hannon GJ,  Beach DH;
XX
DR   WPI; 2000-400055/34.
DR   N-PSDB; AAA29389.
XX
PT   New method for increasing the proliferative capacity of cell lines
PT   comprises administering agents reversibly activating telomerase activity
PT   and reversibly inactivating Rb/INk4 and/or p53 pathways useful in
PT   treating age related diseases.
XX
PS   Claim 5; Page 120; 123pp; English.
XX
CC   The invention concerns methods and reagents for extending the life-span,
CC   e.g. the number of mitotic divisions, of a cell. The method relies on
CC   activation of a telomerase activity and inhibition of one or both of a
CC   retinoblastoma (Rb)/INK4 pathway or a p53 pathway. Phosphorylation of Rb
CC   by cyclin-dependent kinases, cdk4 and cdk6, releases the cells into the
CC   division cycle. Binding of INK4 family members, e.g. the tumour
CC   suppressor p16INK4a, inhibits kinase activity and results in growth
CC   arrest. Rb inactivators can selectively and reversibly inactivate an
CC   Rb/INK4 pathway, especially an Rb/p16INK4a pathway. The oncoprotein MDM2
CC   is a cellular inhibitor of Rb/E2F function and the p53 tumour suppressor
CC   and can also be used in the methods. Other molecules which can be used
CC   include cdk4 or cdk6 mutants. In particular, a cdk4 mutant is one which
CC   differs from at one or more of residues K22, R24, H95 and/or D97.
CC   Additional constructs include a papilloma virus E7 protein, or other
CC   viral oncoprotein which bypasses Rb and/or p53. Antisense constructs of
CC   the Rb and p16INK4a genes may also be used. The methods are useful for
CC   increasing the proliferative capacity of cells. The cells are
CC   subsequently of use in pharmaceutical and cosmetic preparations used to
CC   treat conditions related to (premature) ageing, e.g. macular degeneration
CC   and arteriosclerosis. The cells can also be used to replace tumour cell
CC   lines in vitro and for studies on biochemical and physiological aspects
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CC   of growth and differentiation. Long lived (immortal) cells could also be
CC   of use in the production of normal or genetically engineered
CC   biotechnology products
XX
SQ   Sequence 491 AA;

  Query Match             97.1%;  Score 506;  DB 3;  Length 491;
  Best Local Similarity   93.6%;  Pred. No. 2.2e-59;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||| ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 15
AAB48284
ID   AAB48284 standard; protein; 491 AA.
XX
AC   AAB48284;
XX
DT   02-APR-2001  (first entry)
XX
DE   Human MDM2 protein.
XX
KW   S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF;
KW   CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;
KW   Bad; Bcl-2; tumour; cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO200075184-A1.
XX
PD   14-DEC-2000.
XX
PF   05-JUN-2000; 2000WO-US015449.
XX
PR   04-JUN-1999;   99US-0137494P.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Zhang H,  Tsvetkov LM,  Kondo T;
XX
DR   WPI; 2001-061703/07.
DR   N-PSDB; AAC84596.
XX
PT   Modulating polypeptide levels in a cell, diagnosing and treating tumor,
PT   involves altering levels of proteins such as S-phase kinase associated
PT   proteins 1, 2 and cullin/CDC53 proteins.
XX
PS   Claim 5; Page 93-95; 162pp; English.
XX
CC   The invention relates to methods of altering the polypeptide levels in a
CC   cell, using proteins selected from S-phase kinase associated proteins 1
CC   and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the
CC   cullin/ CDC53 family of proteins). The method is useful for altering the
CC   level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2
CC   polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for
CC   detecting tumours, and in monitoring tumor treatment in a mammal. Agents
CC   that modulate interactions between SKP and target proteins are useful for
CC   treating tumours
XX
SQ   Sequence 491 AA;

  Query Match             97.1%;  Score 506;  DB 4;  Length 491;
  Best Local Similarity   93.6%;  Pred. No. 2.2e-59;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||| ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


Search completed: January 27, 2005, 18:06:15
Job time : 80.8 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:52:56 ; Search time 19.8 Seconds
(without alignments)
529.678 Million cell updates/sec

Title: US-10-822-254-4
Perfect score: 521
Sequence: 1 SQIPASEQETXVRPKPXLLK.....NLVVVNQQESSDSGTSVSEN 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	506	97.1	491	1	S24354	p53-binding protei
2	446.5	85.7	489	2	S15349	mdm2 protein - mou
3	266.5	51.2	489	2	S71955	MDM2-like p53-bind
4	71	13.6	838	2	I45557	eyeless, long form
5	68	13.1	683	2	T38254	serine/threonine-s
6	68	13.1	685	1	SXBPT4	NAD+-protein ADP-r
7	68	13.1	698	1	S31630	NAD+-protein ADP-r
8	68	13.1	698	1	S31714	NAD+-protein ADP-r
9	66.5	12.8	425	2	T50184	mammalian swi/snf
10	66.5	12.8	517	2	S32169	hypothetical prote
11	66	12.7	181	2	S75415	probable ribosomal
12	66	12.7	187	2	S70186	21K protein - Shig
13	65	12.5	331	2	B84938	flagellar motor sw
14	64.5	12.4	380	2	T32112	hypothetical prote
15	64.5	12.4	447	2	I64002	sodium-translocati
16	64.5	12.4	467	2	T25848	hypothetical prote
17	64.5	12.4	525	2	T15185	hypothetical prote
18	64	12.3	286	2	B97743	exodeoxyribonuclea
19	64	12.3	413	2	E83950	processing protein
20	63.5	12.2	709	2	E64213	DNA topoisomerase
21	63	12.1	337	1	ZHBPG4	gene H protein - p
22	63	12.1	456	2	AG3471	beta-alanine-pyruv
23	62.5	12.0	451	2	F83747	denosylmethionine-
24	62.5	12.0	636	2	H96666	probable phytochro
25	62	11.9	261	2	H71680	exodeoxyribonuclea
26	62	11.9	316	2	F69491	methenyltetrahydro
27	62	11.9	600	2	H81733	DNA primase TC0175
28	62	11.9	1333	2	A37488	Ras guanine nucleo
29	62	11.9	1336	2	S25716	Ras guanine nucleo
30	61	11.7	5138	2	B96695	hypothetical prote
31	60.5	11.6	226	2	AC0629	conserved hypothet
32	60.5	11.6	274	1	C69362	conserved hypothet
33	60.5	11.6	339	2	A90395	conserved hypothet
34	60.5	11.6	660	2	F85069	hypothetical prote
35	60.5	11.6	882	2	S57704	hypothetical prote
36	60.5	11.6	1292	2	F64237	DNA-directed RNA p
37	60.5	11.6	1538	2	G64922	probable ATP-depen
38	60.5	11.6	1793	2	T47897	guanine nucleotide
39	60	11.5	206	1	XUBYMC	methylated-DNA-[pr
40	60	11.5	218	2	B64242	hypothetical prote
41	60	11.5	377	2	F97250	proline/glycine be
42	60	11.5	391	2	S14577	asparagine-rich pr
43	60	11.5	439	2	A96981	probable Zn-depend
44	60	11.5	855	2	B89472	protein ZC53.4 [im
45	59.5	11.4	245	2	F64347	hypothetical prote

ALIGNMENTS

RESULT 1
S24354
p53-binding protein mdm2 - human
N;Alternate names: mdm-2 oncogene; mouse double minute 2 homolog; p53-associated phospho
N;Contains: p53-binding protein mdm2, splice form A
C;Species: Homo sapiens (man)
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C;Accession: S24354; S57338; G02026
R;Oliner, J.D.; Kinzler, K.W.; Meltzer, P.S.; George, D.L.; Vogelstein, B.
Nature 358, 80-83, 1992
A;Title: Amplification of a gene encoding a p53-associated protein in human sarcomas.
A;Reference number: S24354; MUID:92310576; PMID:1614537
A;Accession: S24354
A;Molecule type: mRNA
A;Residues: 1-491 <OLI>
A;Cross-references: EMBL:Z12020; NID:g35211; PIDN:CAA78055.1; PID:g35212
R;Zauberman, A.; Flusberg, D.; Haupt, Y.; Barak, Y.; Oren, M.
Nucleic Acids Res. 23, 2584-2592, 1995
A;Title: A functional p53-responsive intronic promoter is contained within the human mdm
A;Reference number: S57338; MUID:95380270; PMID:7651818
A;Accession: S57338
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-16,'P',18-24 <ZAU>
A;Cross-references: EMBL:U28935; NID:g904033; PIDN:AAA82237.1; PID:g904034
R;Lunec, J.
submitted to the EMBL Data Library, August 1995
A;Description: Multiple alternate spliced mdm2 transcripts with loss of p53 binding doma
A;Reference number: G09070
A;Accession: G02026
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-27,223-491 <LUN>
A;Cross-references: EMBL:U33199; NID:g992676; PIDN:AAA75514.1; PID:g992677
A;Experimental source: splice form A
C;Genetics:
A;Gene: GDB:MDM2
A;Cross-references: GDB:250456; OMIM:164785
A;Map position: 12q14.3-12q15
C;Superfamily: human p53-binding protein mdm2
C;Keywords: alternative splicing; oncogene; phosphoprotein
F;1-491/Product: p53-binding protein mdm-2 #status predicted <MAT1>
F;1-27,223-491/Product: p53-binding protein mdm-2, splice form A #status predicted <MAT2

Query Match 97.1%; Score 506; DB 1; Length 491;
Best Local Similarity 93.6%; Pred. No. 8.3e-50;
Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              ||||||||||  ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76
```

```
Qy          61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
               |||| ||||||| |||||||||||||| ||||||||||||||||||||
Db          77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 2
S15349
mdm2 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S15349
R;Fakharzadeh, S.S.; Trusko, S.P.; George, D.L.
EMBO J. 10, 1565-1569, 1991
A;Title: Tumorigenic potential associated with enhanced expression of a gene that is amp
A;Reference number: S15349; MUID:91224107; PMID:2026149
A;Accession: S15349
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-489 <FAK>
A;Cross-references: UNIPROT:P23804; EMBL:X58876; NID:g53038; PIDN:CAA41684.1; PID:g53039
C;Genetics:
A;Gene: mdm2
C;Superfamily: human p53-binding protein mdm2

  Query Match             85.7%;  Score 446.5;  DB 2;  Length 489;
  Best Local Similarity   81.7%;  Pred. No. 5.1e-43;
  Matches   89;  Conservative    7;  Mismatches   10;  Indels    3;  Gaps    1;

Qy           1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
               |||||||||| ||||| |||||||||| |||||||:: |:||||||||||||||||||
Db          17 SQIPASEQETLVRPKPLLLKLLKSVGAQNDTYTMKEIIFYIGQYIMTKRLYDEKQQHIVY 76

Qy          61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
               |||| |||:||| |||||||||| || |||| |:||   |||||:||:
Db          77 CSNDLLGDVFGVPSFSVKEHRKIYAMIYRNLVAVSQQ---DSGTSLSES 122


RESULT 3
S71955
MDM2-like p53-binding protein MDMX - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
C;Accession: S71955
R;Shvarts, A.; Steegenga, W.T.; Riteco, N.; van Laar, T.; Dekker, P.; Bazuine, M.; van H
EMBO J. 15, 5349-5357, 1996
A;Title: MDMX: a novel p53-binding protein with some functional properties of MDM2.
A;Reference number: S71955; MUID:97050840; PMID:8895579
A;Accession: S71955
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-489 <SHV>
A;Cross-references: UNIPROT:O35618; EMBL:AF007110; NID:g2253388; PIDN:AAB62927.1; PID:g2
C;Genetics:
A;Gene: MDMX
C;Function:
A;Description: inhibits transcription activation function of tumour suppressor protein p
C;Superfamily: human p53-binding protein mdm2

  Query Match             51.2%;  Score 266.5;  DB 2;  Length 489;
  Best Local Similarity   51.4%;  Pred. No. 1.7e-22;
  Matches   54;  Conservative   16;  Mismatches   24;  Indels   11;  Gaps    1;

Qy           5 ASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVXCSND 64
               :||| : |||| |||:| : ||| : :|||||: ||||||| |:|||:::||:| |  |
Db          20 SSEQISQVRPKLQLLKILHAAGAQGEVFTMKEVMHYLGQYIMVKQLYDQQEQHMVYCGGD 79

Qy          65 XLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
               |||| |  |||||:   :| |: :|||           || | |
Db          80 LLGDLLGCQSFSVKDPSPLYDMLRKNLV----------TSASNN 113


RESULT 4
I45557
eyeless, long form - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 16-Aug-2004
C;Accession: I45557
R;Quiring, R.; Walldorf, U.; Kloter, U.; Gehring, W.J.
Science 265, 785-789, 1994
A;Title: Homology of the eyeless gene of Drosophila to the Small eye gene in mice and An
A;Reference number: A54584; MUID:94323757; PMID:7914031
A;Accession: I45557
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-838 <RES>
A;Cross-references: EMBL:X79493; NID:g641809; PIDN:CAA56038.1; PID:g641810
C;Genetics:
A;Gene: FlyBase:ey
A;Cross-references: FlyBase:FBgn0005558
A;Introns: 37/1; 92/2; 152/3; 371/1; 429/1; 521/1; 639/2
C;Superfamily: homeobox homology; paired box homology
C;Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulati
F;37-161/Domain: paired box homology <PBH>
F;412-468/Domain: homeobox homology <HOX>

  Query Match             13.6%;  Score 71;  DB 2;  Length 838;
  Best Local Similarity   24.1%;  Pred. No. 6.5;
  Matches   27;  Conservative   17;  Mismatches   40;  Indels   28;  Gaps    5;

Qy           1 SQIPASEQET-XVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQY------IMTKRLYDE 53
               |:|    ||  :||        :::|  |       ||:  : ||      |    : |
Db          87 SKILGRYYETGSIRP--------RAIGGSKPRVATAEVVSKISQYKRECPSIFAWEIRDR 138

Qy          54 KQQHIVXCSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTS 105
               |  | |:|| :  :  :          : |||   :|:|: ||:|
Db         139 LLQENV-CTNDNIPSVSSI----------NRVLRNLAAQKEQQSTGSGSS 177


RESULT 5
T38254
serine/threonine-specific protein kinase plo1 (EC 2.7.1.-) - fission yeast (Schizosaccha
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2004
C;Accession: T38254; T45128
R;Brown, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, August 1995
A;Reference number: Z21781
A;Accession: T38254
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-683 <BRO>
A;Cross-references: UNIPROT:P50528; EMBL:Z98559; PIDN:CAB11167.1; GSPDB:GN00066; SPDB:SP
A;Experimental source: strain 972h-; cosmid c23C11
R;Ohkura, H.; Hagan, I.M.; Glover, D.M.
Genes Dev. 9, 1059-1073, 1995
A;Title: The conserved Schizosaccharomyces pombe kinase plo1, required to form a bipolar
A;Reference number: Z22921; MUID:95262899; PMID:7744248
A;Accession: T45128
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-683 <OHK>
A;Cross-references: EMBL:X85758; NID:g887640; PIDN:CAA59766.1; PID:g887641
A;Experimental source: strain 972 derivative
C;Genetics:
A;Gene: plo1; SPAC23C11.16
A;Map position: 1
C;Function:
A;Description: required to form a bipolar spindle and early in the regulatory cascade th
C;Superfamily: protein kinase homology
C;Keywords: phosphotransferase; protein kinase

  Query Match             13.1%;  Score 68;  DB 2;  Length 683;
  Best Local Similarity   22.4%;  Pred. No. 11;
  Matches   24;  Conservative   20;  Mismatches   37;  Indels   26;  Gaps    4;

Qy           4 PASEQETXVRPKPXLLKLLKSVGAQ----------KDTYTMKEVLXYLGQYIMTKRLY 51
```

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              |||:    :| |  |||  ||   |             |   :    : ::  |: |
Db        551 PASKVPESIRSKLQLLKHFKSYMGQNLSKAVQDESFEKPKNSTSNTMLFMQHYLRT---- 606

Qy         52 DEKQQHIVXCSNDXLGDLFGVXSFSVKEHRK-IYTMIXRNLVVVNQQ 97
                :|  :   ||       |:  |:  :||| : :   | ::|::::
Db        607 --RQAIMFRLSN-------GIFQFNFLDHRKVVISSTARKIIVLDKE 644


RESULT 6
SXBPT4
NAD+-protein ADP-ribosyltransferase (EC 2.4.2.-) precursor - phage T4
C;Species: phage T4
A;Note: host Escherichia coli
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C;Accession: JU0096
R;Hilse, D.; Koch, T.; Rueger, W.
Nucleic Acids Res. 17, 6731, 1989
A;Title: Nucleotide sequence of the alt gene of bacteriophage T4.
A;Reference number: JU0096; MUID:89386005; PMID:2506526
A;Accession: JU0096
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-685 <HIL>
A;Cross-references: UNIPROT:P12726
C;Comment: This enzyme catalyzes the ADP-ribosylation of one of the two alpha-subunits c
C;Genetics:
A;Gene: alt
C;Superfamily: phage T4 NAD-protein ADP-ribosyltransferase
C;Keywords: glycosyltransferase; pentosyltransferase
F;7-685/Product: NAD-protein ADP-ribosyltransferase #status predicted <MAT>

  Query Match             13.1%;  Score 68;  DB 1;  Length 685;
  Best Local Similarity   27.0%;  Pred. No. 11;
  Matches   27;  Conservative   22;  Mismatches   37;  Indels   14;  Gaps    6;

Qy         18 LLKLLKS--VGAQKDTYTMKEVLXYL---GQYIMTKRL--YDEKQQHI-VXCSNDXLGDL 69
              :|::|||    |  :    : : |      |:|:: | |  ||:|  :| :   |  | |:
Db        111 MLRILKSKTAGQARQIQVIADRLIRSRSGGRYVLLKELWDYDKKYAYILIHRKNVSLEDI 170

Qy         70 FGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
               ||   | :   |: : :    | :|:    |:|  |::|
Db        171 PGVPEISTELFTKVESKVGD--VYINK----DTGAQVTKN 204


RESULT 7
S31630
NAD+-protein ADP-ribosyltransferase (EC 2.4.2.-) precursor - phage T2
C;Species: phage T2
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S31630
R;Koch, T.; Rueger, W.
submitted to the EMBL Data Library, December 1992
A;Description: The ADP-ribosyltransferase of bacteriophages T2, T4 and T6: Sequencing of
A;Reference number: S31630
A;Accession: S31630
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-698 <KOC>
A;Cross-references: UNIPROT:Q38424; EMBL:X69893; NID:g15187; PIDN:CAA49517.1; PID:g15188
C;Superfamily: phage T4 NAD-protein ADP-ribosyltransferase
C;Keywords: glycosyltransferase; NAD; pentosyltransferase

  Query Match             13.1%;  Score 68;  DB 1;  Length 698;
  Best Local Similarity   27.0%;  Pred. No. 12;
  Matches   27;  Conservative   22;  Mismatches   37;  Indels   14;  Gaps    6;

Qy         18 LLKLLKS--VGAQKDTYTMKEVLXYL---GQYIMTKRL--YDEKQQHI-VXCSNDXLGDL 69
              :|::|||    |  :    : : |      |:|:: | |  ||:|  :| :   |  | |:
Db        112 MLRILKSKTAGQARQIQVIADRLIRSRSGGRYVLLKELWDYDKKYAYILIHRKNVSLEDI 171

Qy         70 FGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
               ||   | :   |: : :    | :|:    |:|  |::|
Db        172 PGVPEISTELFTKVESKVGD--VYINK----DTGAQVTKN 205


RESULT 8
S31714
NAD+-protein ADP-ribosyltransferase (EC 2.4.2.-) precursor - phage T6
C;Species: phage T6
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S31714
R;Koch, T.; Rueger, W.
submitted to the EMBL Data Library, December 1992
A;Description: The ADP-ribosyltransferase of bacteriophages T2, T4 and T6: Sequencing of
A;Reference number: S31630
A;Accession: S31714
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-698 <KOC>
A;Cross-references: UNIPROT:Q38433; EMBL:X69894; NID:g15422; PIDN:CAA49518.1; PID:g15423
C;Superfamily: phage T4 NAD-protein ADP-ribosyltransferase
C;Keywords: glycosyltransferase; NAD; pentosyltransferase

  Query Match             13.1%;  Score 68;  DB 1;  Length 698;
  Best Local Similarity   27.0%;  Pred. No. 12;
  Matches   27;  Conservative   22;  Mismatches   37;  Indels   14;  Gaps    6;

Qy         18 LLKLLKS--VGAQKDTYTMKEVLXYL---GQYIMTKRL--YDEKQQHI-VXCSNDXLGDL 69
              :|::|||    |  :    : : |      |:|:: | |  ||:|  :| :   |  | |:
Db        112 MLRILKSKTAGQARQIQVIADRLIRSRSGGRYVLLKELWDYDKKYAYILIHRKNVSLEDI 171

Qy         70 FGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
               ||   | :   |: : :    | :|:    |:|  |::|
Db        172 PGVPEISTELFTKVESKVGD--VYINK----DTGAQVTKN 205


RESULT 9
T50184
mammalian swi/snf complex 60 kda subunit homolog [imported] - fission yeast (Schizosacch
C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C;Accession: T50184
R;Badcock, K.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, February 2000
A;Reference number: Z25044
A;Accession: T50184
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-425 <BAD>
A;Cross-references: UNIPROT:Q9P7S3; EMBL:AL138854; PIDN:CAB72235.1; GSPDB:GN00066; SPDB
A;Experimental source: strain 972h(-); cosmid c23G3
C;Genetics:
A;Gene: SPDB:SPAC23G3.10c
A;Map position: 1

  Query Match             12.8%;  Score 66.5;  DB 2;  Length 425;
  Best Local Similarity   36.8%;  Pred. No. 9.7;
  Matches   14;  Conservative    9;  Mismatches   14;  Indels    1;  Gaps    1;

Qy         33 TMKEVLXYLGQYIMTKRLYDEKQQHIVXCSNDXLGDLF 70
              |  ::: || |||   || | ::: :: | :  | |||
Db        222 TRPDIVSYLWQYIKFHRLQDMEEKRLINC-DKALRDLF 258


RESULT 10
S32169
hypothetical protein 2 - Myxococcus xanthus
C;Species: Myxococcus xanthus
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S32169; S67952
R;Botella, J.; Murillo, F.; Ruiz-vazquez, R.
submitted to the EMBL Data Library, March 1993
A;Description: Nucleotide and deduced protein sequences of a carotenoid gene cluster in
A;Reference number: S32168
A;Accession: S32169
A;Molecule type: DNA
```

```
A;Residues: 1-517 <BOT>
A;Cross-references: UNIPROT:P54979; EMBL:Z21955; NID:g577589; PIDN:CAA79956.1; PID:g2882
A;Experimental source: strain DK1050
R;Botella, J.A.; Murillo, F.J.; Ruiz-Vazquez, R.
Eur. J. Biochem. 233, 238-248, 1995
A;Title: A cluster of structural and regulatory genes for light-induced carotenogenesis
A;Reference number: S67950; MUID:96061955; PMID:7588751
A;Accession: S67952
A;Molecule type: DNA
A;Residues: 9-37;462-488 <BOW>
C;Superfamily: phytoene dehydrogenase

  Query Match             12.8%;  Score 66.5;  DB 2;  Length 517;
  Best Local Similarity   30.3%;  Pred. No. 12;
  Matches   23;  Conservative    4;  Mismatches   40;  Indels    9;  Gaps    2;

Qy           9 ETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVXCSNDXLGD 68
               |  : ||   ||       :|  ||    : |||     || | |   | |    |  |
Db         289 EKLLDPKATTLK-----RKEKLRYTSSGYMLYLGM----KRRYPELLHHNVVFGRDYKGS 339

Qy          69 LFGVXSFSVKEHRKIY 84
                 :  | | |    |
Db         340 FDDIFEFRVPEDPSFY 355


RESULT 11
S75415
probable ribosomal protein S4 - Sulfolobus solfataricus
N;Alternate names: protein c04049
C;Species: Sulfolobus solfataricus
C;Date: 11-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C;Accession: S75415
R;Sensen, C.W.; Klenk, H.P.; Singh, R.K.; Allard, G.; Chan, C.C.Y.; Liu, Q.Y.; Penny, S.
Mol. Microbiol. 22, 175-191, 1996
A;Title: Organizational characteristics and information content of an archaeal genome: 1
A;Reference number: S73076; MUID:97055432; PMID:8899719
A;Accession: S75415
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-181 <SEN>
A;Cross-references: UNIPROT:P95987; EMBL:Y08257; NID:g1707772; PIDN:CAA69529.1; PID:g170
A;Experimental source: strain P2
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1996
C;Superfamily: rat ribosomal protein S9
C;Keywords: protein biosynthesis; ribosome

  Query Match             12.7%;  Score 66;  DB 2;  Length 181;
  Best Local Similarity   22.4%;  Pred. No. 4.2;
  Matches   28;  Conservative   17;  Mismatches   38;  Indels   42;  Gaps    3;

Qy           9 ETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRL-------------YDEKQ 55
               |  || |  : ||||    :|:| |: ::|    | :: :||             |  :|
Db          65 ERAVREKQLVGKLLKMGLLKKETATVDDILSLTEQDLLERRLQTIVYKKGLSNTIYQARQ 124

Qy          56 -----------------QHIVXCSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQE 98
                              :||    : | | :   ||  :              |::|||
Db         125 LITHGHIAVNGKRVTSPGYIVNVDEENLIDYYVTSSFKSRP-----------PVMSQQE 172

Qy          99 SSDSG 103
                 : |
Db         173 GGEIG 177


RESULT 12
S70186
21K protein - Shigella flexneri
C;Species: Shigella flexneri
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 09-Jul-2004
C;Accession: S70186
R;Uchiya, K.; Tobe, T.; Komatsu, K.; Suzuki, T.; Watarai, M.; Fukuda, I.; Yoshikawa, M.;
Mol. Microbiol. 17, 241-250, 1995
A;Title: Identification of a novel virulence gene, virA, on the large plasmid of Shigell
A;Reference number: S70186; MUID:96079274; PMID:7494473
A;Accession: S70186
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-187 <UCH>
A;Cross-references: UNIPROT:Q52296; EMBL:D26468; NID:g992954; PIDN:BAA05481.1; PID:d1006
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1994

  Query Match             12.7%;  Score 66;  DB 2;  Length 187;
  Best Local Similarity   21.6%;  Pred. No. 4.3;
  Matches   21;  Conservative   15;  Mismatches   33;  Indels   28;  Gaps    3;

Qy          23 KSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQ---------------HIVXCSNDXL 66
               :|  ||:| :  ||:|           |:||| |                 :  |:   |
Db          40 RSARAQRDDWLKKEIL----------RVYDENHQVYAVRKVWHQLLREGIRVARCTVARL 89

Qy          67 GDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSG 103
                 : |:    |   :|::| : |  |    : :   |
Db          90 MAVMGLA--GVLRGKKVHTTVSRKAVAAGDRVNRHQG 124


RESULT 13
B84938
flagellar motor switch protein fliG [imported] - Buchnera sp. (strain APS)
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 24-Aug-2001
C;Accession: B84938
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A
A;Reference number: A84930; MUID:20445173; PMID:10993077
A;Accession: B84938
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-331 <STO>
A;Cross-references: GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
C;Genetics:
A;Gene: fliG; BU074
C;Superfamily: flagellar switch protein fliG

  Query Match             12.5%;  Score 65;  DB 2;  Length 331;
  Best Local Similarity   27.1%;  Pred. No. 11;
  Matches   23;  Conservative   16;  Mismatches   28;  Indels   18;  Gaps    3;

Qy          18 LLKLL-KSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVXCSNDXLGDLFGVXSFS 76
               |:|:| |::| :| |  :|| |       |  | |    | : :    :
Db          77 LIKMLTKALGEKKGTSLLKEALEIRNARICIKALNYMKAKQVAFLLD------------ 123

Qy          77 VKEHRKIYTMIXRNLVVVNQQESSD 101
                 ||| :| | |    |: :|: :|::
Db         124 -KEHPQIITTI---LICLNKNQSAE 144


RESULT 14
T32112
hypothetical protein F59E11.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T32112
R;Bradshaw, H.
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid F59E11.
A;Reference number: Z21124
A;Accession: T32112
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-380 <BRA>
A;Cross-references: UNIPROT:Q22556; EMBL:AF016685; PIDN:AAB66222.1; GSPDB:GN00023; CESP
A;Experimental source: strain Bristol N2; clone F59E11
C;Genetics:
A;Gene: CESP:F59E11.8
A;Map position: 5
A;Introns: 72/2; 92/1; 118/3; 191/3; 223/3; 345/3
```

```
  Query Match             12.4%;  Score 64.5;  DB 2;  Length 380;
  Best Local Similarity   28.7%;  Pred. No. 14;
  Matches   27;  Conservative   18;  Mismatches   24;  Indels   25;  Gaps    6;

Qy          1 SQIPASEQETXVRPKPXLLKLL---------KSVGAQKDTYTMKEVLXYLGQYIMTKRLY 51
              ::|  | |:|  |    || :|         :   | : :| : ::|    ||   | |
Db        296 NKIGGSMQKTTER----LLNILADNLHEYYVEQKDATRYSYRLTKILKISQQY---KTLM 348

Qy         52 DEKQQHIVXCSNDXLGDLFGVXSFSVK-EHRKIY 84
              :||::       : |||:||  :| ||  | :|:
Db        349 EEKRR------TEVLGDVFG--AFRVKWSHSEIF 374


RESULT 15
I64002
sodium-translocating NADH dehydrogenase (ubiquinone) (EC 1.6.5.-) alpha chain HI0164 [si
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C;Accession: I64002; A64003
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J
, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: I64002
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-447 <TIGR>
A;Cross-references: UNIPROT:P43955; GB:L42023; TIGR:HI0164; GB:U32702; NID:g1573118; PID
A;Note: the sequence is revised in GenBank entry U32702, PID:g1573122
C;Superfamily: Vibrio alginolyticus sodium-translocating NADH dehydrogenase (ubiquinone)
C;Keywords: oxidoreductase

  Query Match             12.4%;  Score 64.5;  DB 2;  Length 447;
  Best Local Similarity   25.0%;  Pred. No. 17;
  Matches   28;  Conservative   16;  Mismatches   41;  Indels   27;  Gaps    5;

Qy          1 SQIPASEQE-------TXVRPKPXL---LKLLKSVGAQKDTY--TMKEVLXYLGQYIMTK 48
              | || :: |       | | |   :   :  :  || ||  :    ::|:  :|:   |
Db        198 SNIPTADLENLQIHDFTGVHPAGLVGTHIHFIDPVGIQKTVWHINYQDVIA-VGKLFTTG 256

Qy         49 RLYDEKQQHIVXCSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESS 100
               || |:               :  :    ||| | : | |  ||  : | | |
Db        257 ELYSER-------------VISLAGPQVKEPRLVRTTIGANLSQLTQNELS 294


Search completed: January 27, 2005, 18:15:09
Job time : 20.8 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:51:46 ; Search time 84.6 Seconds
(without alignments)
741.322 Million cell updates/sec

Title: US-10-822-254-4
Perfect score: 521
Sequence: 1 SQIPASEQETXVRPKPXLLK.....NLVVVNQQESSDSGTSVSEN 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	506	97.1	166	2	Q8NDW2	Q8ndw2 homo sapien
2	506	97.1	195	2	Q96DS4	Q96ds4 homo sapien
3	506	97.1	243	2	Q8TE47	Q8te47 homo sapien
4	506	97.1	491	1	MDM2_HUMAN	Q00987 homo sapien
5	506	97.1	491	2	AAP35922	Aap35922 homo sapi
6	506	97.1	491	2	AAH67077	Aah67077 homo sapi
7	494	94.8	487	1	MDM2_CANFA	P56950 canis famil
8	494	94.8	487	2	Q9GMZ6	Q9gmz6 canis famil
9	494	94.8	491	1	MDM2_HORSE	P56951 equus cabal
10	491	94.2	491	2	Q7YRZ8	Q7yrz8 felis silve
11	456	87.5	436	2	Q8WYJ2	Q8wyj2 homo sapien
12	446.5	85.7	489	1	MDM2_MOUSE	P23804 mus musculu
13	446.5	85.7	489	2	Q91XK7	Q91xk7 m mus muscu
14	429	82.3	118	2	Q8WYJ3	Q8wyj3 homo sapien
15	428.5	82.2	466	1	MDM2_MESAU	Q60524 mesocricetu
16	393	75.4	325	2	Q9PVL2	Q9pvl2 gallus gall
17	368	70.6	173	2	Q8TE46	Q8te46 homo sapien
18	344	66.0	473	1	MDM2_XENLA	P56273 xenopus lae
19	344	66.0	473	2	Q6GMB5	Q6gmb5 xenopus lae
20	343	65.8	482	2	Q6P3Q9	Q6p3q9 xenopus tro
21	343	65.8	482	2	AAH63898	Aah63898 xenopus t
22	314.5	60.4	105	2	Q8NDW0	Q8ndw0 homo sapien
23	290	55.7	426	2	Q9GK41	Q9gk41 canis famil
24	280.5	53.8	445	1	MDM2_BRARE	O42354 brachydanio
25	280.5	53.8	445	2	AAM00198	Aam00198 brachydan
26	270	51.8	491	2	Q7ZUW7	Q7zuw7 brachydanio
27	266.5	51.2	489	1	MDM4_MOUSE	O35618 mus musculu
28	263.5	50.6	489	2	Q9CYG1	Q9cyg1 m mus muscu
29	263	50.5	475	2	Q7ZYI3	Q7zyi3 xenopus lae
30	262.5	50.4	446	2	Q8WYJ1	Q8wyj1 homo sapien
31	257	49.3	490	2	Q99L86	Q99186 mus musculu
32	251.5	48.3	134	2	Q6PHL8	Q6phl8 xenopus lae
33	251.5	48.3	134	2	AAH56503	Aah56503 xenopus l
34	241	46.3	153	2	Q6MZR7	Q6mzr7 homo sapien
35	241	46.3	153	2	CAE45961	Cae45961 homo sapi
36	241	46.3	490	2	AAH67299	Aah67299 homo sapi
37	239	45.9	490	1	MDM4_HUMAN	O15151 homo sapien
38	206	39.5	69	2	Q86WA4	Q86wa4 homo sapien
39	199	38.2	66	2	Q96DS3	Q96ds3 homo sapien
40	196	37.6	70	2	Q86WA3	Q86wa3 homo sapien
41	184	35.3	95	2	Q96DS1	Q96ds1 homo sapien
42	168	32.2	159	2	Q96DS0	Q96ds0 homo sapien
43	167	32.1	70	2	Q8NDW1	Q8ndw1 homo sapien
44	166	31.9	60	2	Q96DS5	Q96ds5 homo sapien
45	166	31.9	130	2	Q9H4C3	Q9h4c3 homo sapien

ALIGNMENTS

RESULT 1
Q8NDW2
ID Q8NDW2 PRELIMINARY; PRT; 166 AA.
AC Q8NDW2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE P53-binding protein.
GN Name=MDM2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bartel F., Pinkert D., Kappler M., Bache M., Schmidt H., Taubert H.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ491698; CAD36959.1; -.
DR HSSP; Q9UMT8; 1YCR.
DR GO; GO:0005634; C:nucleus; IEA.
DR InterPro; IPR010984; MDM2.
DR InterPro; IPR003121; SWIB_MDM2.
DR Pfam; PF02201; SWIB; 1.
SQ SEQUENCE 166 AA; 18900 MW; FA6B5BA18E85040D CRC64;

Query Match 97.1%; Score 506; DB 2; Length 166;
Best Local Similarity 93.6%; Pred. No. 2.4e-50;
Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| |||||||| |||||||||||||| ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125
```

RESULT 2
Q96DS4
ID Q96DS4 PRELIMINARY; PRT; 195 AA.
AC Q96DS4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MDM2 variant FB26.
GN Name=MDM2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Rhabdomyosarcoma tumor;

```
RA   Bartel F., Taylor A.C., Taubert H., Harris L.C.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF385323; AAL13243.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB_MDM2.
DR   Pfam; PF02201; SWIB; 1.
SQ   SEQUENCE   195 AA;  22161 MW;  4987AE567DB12D5D CRC64;

  Query Match             97.1%;  Score 506;  DB 2;  Length 195;
  Best Local Similarity   93.6%;  Pred. No. 2.9e-50;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||| ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 3
Q8TE47
ID   Q8TE47      PRELIMINARY;      PRT;   243 AA.
AC   Q8TE47;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   MDM2 isoform KB9 protein.
GN   Name=MDM2 isoform KB9;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymphocytes;
RA   Bartel F., Pinkert D., Kappler M., Bache M., Schmidt H., Taubert H.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ430612; CAD23251.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR   GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   GO; GO:0016567; P:protein ubiquitination; IEA.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB_MDM2.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
SQ   SEQUENCE   243 AA;  27317 MW;  9EB5D0142CF185A2 CRC64;

  Query Match             97.1%;  Score 506;  DB 2;  Length 243;
  Best Local Similarity   93.6%;  Pred. No. 3.6e-50;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||| ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 4
MDM2_HUMAN
ID   MDM2_HUMAN     STANDARD;      PRT;   491 AA.
AC   Q00987; Q13226; Q13297; Q13298; Q13299; Q13300; Q13301; Q9UGI3;
AC   Q9UMT8;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein
DE   Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Hdm2).
GN   Name=MDM2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM MDM2).
RX   MEDLINE=92310576; PubMed=1614537;
RA   Oliner J.D., Kinzler K.W., Meltzer P.S., George D.L., Vogelstein B.;
RT   "Amplification of a gene encoding a p53-associated protein in human
RT   sarcomas.";
RL   Nature 358:80-83(1992).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS MDM2-A; -B; -C; -D AND -E).
RC   TISSUE=Ovarian carcinoma;
RX   MEDLINE=96313107; PubMed=8705862;
RA   Sigalas I., Calvert A.H., Anderson J.J., Neal D.E., Lunec J.;
RT   "Alternatively spliced mdm2 transcripts with loss of p53 binding
RT   domain sequences: transforming ability and frequent detection in human
RT   cancer.";
RL   Nat. Med. 2:912-917(1996).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM MDM2-ALPHA).
RX   MEDLINE=20065171; PubMed=10597303;
RA   Veldhoen N., Metcalfe S., Milner J.;
RT   "A novel exon within the mdm2 gene modulates translation initiation in
RT   vitro and disrupts the p53-binding domain of mdm2 protein.";
RL   Oncogene 18:7026-7033(1999).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM MDM2).
RA   Rieder M.J., Livingston R.J., Braun A.C., Montoya M.A., Chung M.-W.,
RA   Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA   Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RT   "NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department
RT   of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM MDM2).
RC   TISSUE=Muscle;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [6]
RP   SEQUENCE OF 6-491 FROM N.A. (ISOFORM MDM2-A1).
RA   Liang H., Atkins H., Abdel-Fattah R., Suaeyun R., Lunec J.;
RT   "Genomic organisation of the human MDM2 oncogene and relationship to
RT   its alternatively spliced mRNA's.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
RN   [7]
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RP   SEQUENCE OF 1-24 FROM N.A.
RX   MEDLINE=95380270; PubMed=7651818;
RA   Zauberman A., Flusberg D., Haupt Y., Barak Y., Oren M.;
RT   "A functional p53-responsive intronic promoter is contained within the
RT   human mdm2 gene.";
RL   Nucleic Acids Res. 23:2584-2592(1995).
RN   [8]
RP   SEQUENCE OF 1-9 FROM N.A.
RX   MEDLINE=97413643; PubMed=9270029;
RA   Landers J.E., Cassel S.L., George D.L.;
RT   "Translational enhancement of mdm2 oncogene expression in human tumor
RT   cells containing a stabilized wild-type p53 protein.";
RL   Cancer Res. 57:3562-3568(1997).
RN   [9]
RP   SEQUENCE OF 301-481 FROM N.A.
RX   MEDLINE=20542019; PubMed=11087894;
RA   Taubert H., Kappler M., Meye A., Bartel F., Schlott T.,
RA   Lautenschlaeger C., Bache M., Schmidt H., Wuerl P.;
RT   "A MboII polymorphism in exon 11 of the human MDM2 gene occuring in
RT   normal blood donors and in soft tissue sarcoma patients: an indication
RT   for an increased cancer susceptibility?";
RL   Mutat. Res. 456:39-44(2000).
RN   [10]
RP   MUTAGENESIS OF CYS-464.
RX   MEDLINE=98111004; PubMed=9450543;
RA   Honda R., Tanaka H., Yasuda H.;
RT   "Oncoprotein MDM2 is a ubiquitin ligase E3 for tumor suppressor p53.";
RL   FEBS Lett. 420:25-27(1997).
RN   [11]
RP   MUTAGENESIS OF CYS-449.
RX   MEDLINE=20190101; PubMed=10723139;
RA   Honda R., Yasuda H.;
RT   "Activity of MDM2, a ubiquitin ligase, toward p53 or itself is
RT   dependent on the RING finger domain of the ligase.";
RL   Oncogene 19:1473-1476(2000).
RN   [12]
RP   MUTAGENESIS.
RX   MEDLINE=20187618; PubMed=10722742;
RA   Fang S., Jensen J.P., Ludwig R.L., Vousden K.H., Weissman A.M.;
RT   "Mdm2 is a RING finger-dependent ubiquitin protein ligase for itself
RT   and p53.";
RL   J. Biol. Chem. 275:8945-8951(2000).
RN   [13]
RP   MUTAGENESIS OF CYS-441 AND CYS-478.
RX   MEDLINE=20076498; PubMed=10608892;
RA   Sharp D.A., Kratowicz S.A., Sank M.J., George D.L.;
RT   "Stabilization of the MDM2 oncoprotein by interaction with the
RT   structurally related MDMX protein.";
RL   J. Biol. Chem. 274:38189-38196(1999).
RN   [14]
RP   NUCLEOLAR LOCALIZATION SIGNAL.
RX   MEDLINE=20173879; PubMed=10707090;
RA   Lohrum M.A.E., Ashcroft M., Kubbutat M.H.G., Vousden K.H.;
RT   "Identification of a cryptic nucleolar-localization signal in MDM2.";
RL   Nat. Cell Biol. 2:179-181(2000).
RN   [15]
RP   PHOSPHORYLATION BY ATM.
RX   MEDLINE=20079591; PubMed=10611322;
RA   Khosravi R., Maya R., Gottlieb T., Oren M., Shiloh Y., Shkedy D.;
RT   "Rapid ATM-dependent phosphorylation of MDM2 precedes p53 accumulation
RT   in response to DNA damage.";
RL   Proc. Natl. Acad. Sci. U.S.A. 96:14973-14977(1999).
RN   [16]
RP   X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 25-109 IN COMPLEX WITH P53.
RX   MEDLINE=97081050; PubMed=8875929;
RA   Kussie P.H., Gorina S., Marechal V., Elenbaas B., Moreau J.,
RA   Levine A.J., Pavletich N.P.;
RT   "Structure of the MDM2 oncoprotein bound to the p53 tumor suppressor
RT   transactivation domain.";
RL   Science 274:948-953(1996).
CC   -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC       apoptosis by binding its transcriptional activation domain.
CC       Functions as a ubiquitin ligase E3, in the presence of E1 and E2,
CC       toward p53 and itself. Permits the nuclear export of p53 and
CC       targets it for proteasome-mediated proteolysis.
CC   -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity.
CC   -!- SUBUNIT: Binds p53, p73, ARF(P14), ribosomal protein L5 and
CC       specifically to RNA. Can interact also with retinoblastoma protein
CC       (RB), E1A-associated protein EP300 and the E2F1 transcription
CC       factor.
CC   -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed
CC       predominantly in the nucleoplasm. Interaction with ARF(P14)
CC       results in the localization of both proteins to the nucleolus. The
CC       nucleolar localization signals in both ARF(P14) and MDM2 may be
CC       necessary to allow efficient nucleolar localization of both
CC       proteins.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=8;
CC       Name=Mdm2;
CC         IsoId=Q00987-1; Sequence=Displayed;
CC       Name=Mdm2-A;
CC         IsoId=Q00987-2; Sequence=VSP_003208;
CC       Name=Mdm2-A1;
CC         IsoId=Q00987-3; Sequence=VSP_003208, VSP_003214;
CC       Name=Mdm2-B;
CC         IsoId=Q00987-4; Sequence=VSP_003209;
CC       Name=Mdm2-C;
CC         IsoId=Q00987-5; Sequence=VSP_003211;
CC       Name=Mdm2-D;
CC         IsoId=Q00987-6; Sequence=VSP_003210;
CC       Name=Mdm2-E;
CC         IsoId=Q00987-7; Sequence=VSP_003212, VSP_003213;
CC       Name=Mdm2-alpha;
CC         IsoId=Q00987-8; Sequence=VSP_003207;
CC   -!- TISSUE SPECIFICITY: Ubiquitous. Isoforms MDM2-A, -B, -C, -D and -E
CC       are observed in a range of human cancers but absent in normal
CC       tissues.
CC   -!- INDUCTION: By DNA damage.
CC   -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its
CC       G1 arrest and apoptosis functions. It also binds p73 and E2F1.
CC       Region II contains most of a central acidic region required for
CC       interaction with ribosomal protein L5 and a putative C4-type zinc
CC       finger. The RING finger domain which coordinates two molecules of
CC       zinc interacts specifically with RNA whether or not zinc is
CC       present and mediates the hetero-oligomerization with MDM4. It is
CC       also essential for its ubiquitin ligase E3 activity toward p53 and
CC       itself.
CC   -!- PTM: Phosphorylated in response to ionizing radiation in an ATM-
CC       dependent manner.
CC   -!- DISEASE: Seems to be amplified in certain tumors (including soft
CC       tissue sarcomas, osteosarcomas and gliomas). A higher frequency of
CC       splice variants lacking p53 binding domain sequences was found in
CC       late-stage and high-grade ovarian and bladder carcinomas. Four of
CC       the splice variants show loss of p53 binding.
CC   -!- MISCELLANEOUS: MDM2 RING finger mutations that failed to

  Query Match           97.1%;  Score 506;  DB 1;  Length 491;
  Best Local Similarity  93.6%;  Pred. No. 8e-50;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||| ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125

RESULT 5
AAP35922
ID   AAP35922    PRELIMINARY;      PRT;   491 AA.
AC   AAP35922;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
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DE   Mdm2, transformed 3T3 cell double minute 2, p53 binding protein
DE   (Mouse).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA   Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA   Phelan M., Farmer A.;
RT   "Cloning of human full-length CDSs in BD Creator(TM) System Donor
RT   vector.";
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BT007258; AAP35922.1; -.
SQ   SEQUENCE   491 AA;  55232 MW;  F37CE163876BC983 CRC64;

  Query Match             97.1%;  Score 506;  DB 2;  Length 491;
  Best Local Similarity   93.6%;  Pred. No. 8e-50;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||| ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 6
AAH67077
ID   AAH67077    PRELIMINARY;      PRT;   491 AA.
AC   AAH67077;
DT   14-APR-2004 (TrEMBLrel. 27, Created)
DT   14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT   14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle;
RA   Strausberg R.;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC067077; AAH67077.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   491 AA;  55232 MW;  F37CE163876BC983 CRC64;

  Query Match             97.1%;  Score 506;  DB 2;  Length 491;
  Best Local Similarity   93.6%;  Pred. No. 8e-50;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||| ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 7
MDM2_CANFA
ID   MDM2_CANFA     STANDARD;      PRT;   487 AA.
AC   P56950; Q95KN5;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein
DE   Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Cdm2).
GN   Name=MDM2;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE OF 1-484 FROM N.A.
RX   MEDLINE=20218866; PubMed=10754200;
RA   Nasir L., Burr P.D., McFarlane S.T., Gault E., Thompson H.,
RA   Argyle D.J.;
RT   "Cloning, sequence analysis and expression of the cDNAs encoding the
RT   canine and equine homologues of the mouse double minute 2 (mdm2)
RT   proto-oncogene.";
RL   Cancer Lett. 152:9-13(2000).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS MDM2 AND MDM2-ALPHA).
RX   MEDLINE=20065171; PubMed=10597303;
RA   Veldhoen N., Metcalfe S., Milner J.;
RT   "A novel exon within the mdm2 gene modulates translation initiation in
RT   vitro and disrupts the p53-binding domain of mdm2 protein.";
RL   Oncogene 18:7026-7033(1999).
CC   -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC       apoptosis by binding its transcriptional activation domain.
CC       Functions as a ubiquitin ligase E3, in the presence of E1 and E2,
CC       toward p53 and itself. Permits the nuclear export of p53 and
CC       targets it for proteasome-mediated proteolysis (By similarity).
CC   -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity (By
CC       similarity).
CC   -!- SUBUNIT: Binds p53, p73, ARF(P14), ribosomal protein L5 and
CC       specifically to RNA. Can interact also with retinoblastoma protein
CC       (RB), E1A-associated protein EP300 and the E2F1 transcription
CC       factor (By similarity).
CC   -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed
CC       predominantly in the nucleoplasm (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Mdm2;
CC         IsoId=P56950-1; Sequence=Displayed;
CC       Name=Mdm2-alpha;
CC         IsoId=P56950-2; Sequence=VSP_003206;
CC   -!- TISSUE SPECIFICITY: Isoform Mdm2-alpha is present in lymphoid and
CC       testicular tissues.
CC   -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its
CC       G1 arrest and apoptosis functions. It also binds p73 and E2F1.
CC       Region II contains most of a central acidic region required for
CC       interaction with ribosomal protein L5 and a putative C4-type zinc
CC       finger. The RING finger domain which coordinates two molecules of
CC       zinc interacts specifically with RNA whether or not zinc is
CC       present and mediates the hetero-oligomerization with MDM4. It is
```

```
CC       also essential for its ubiquitin ligase E3 activity toward p53 and
CC       itself (By similarity).
CC   -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.
CC   -!- SIMILARITY: Contains 1 RanBP2-type zinc finger.
CC   -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC   -!- SIMILARITY: Contains 1 SWIB domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF100705; AAF67833.1; -.
DR   EMBL; AF322416; AAG42840.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Alternative splicing; Ligase; Metal-binding; Nuclear protein;
KW   Ubl conjugation pathway; Zinc; Zinc-finger.
FT   DOMAIN       27    107       SWIB.
FT   DOMAIN      179    185       Nuclear localization signal (Potential).
FT   DOMAIN      190    202       Nuclear export signal.
FT   DOMAIN      210    304       ARF-binding.
FT   DOMAIN      210    215       Poly-Ser.
FT   DOMAIN      242    331       Region II.
FT   DOMAIN      243    301       Asp/Glu-rich (acidic).
FT   ZN_FING     299    328       RanBP2-type.
FT   ZN_FING     434    475       RING-type.
FT   DOMAIN      462    469       Nucleolar localization signal
FT                                (Potential).
FT   VARSPLIC      1     61       Missing (in isoform Mdm2-alpha).
FT                                /FTId=VSP_003206.
FT   CONFLICT     11     11       G -> D (in Ref. 2).
FT   CONFLICT    238    239       QD -> HH (in Ref. 2).
SQ   SEQUENCE   487 AA;  54696 MW;  60CDB470A32A8E69 CRC64;

  Query Match             94.8%;  Score 494;  DB 1;  Length 487;
  Best Local Similarity   90.8%;  Pred. No. 1.9e-48;
  Matches   99;  Conservative    1;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||||: ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVIFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||| ||||||| | ||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQHEPSDSGTSVSEN 125


RESULT 8
Q9GMZ6
ID   Q9GMZ6      PRELIMINARY;      PRT;   487 AA.
AC   Q9GMZ6;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   MDM2.
GN   Name=mdm2;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Setoguchi A., Tsujimoto H.;
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB031276; BAB11975.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   GO; GO:0005730; C:nucleolus; ISS.
DR   GO; GO:0005654; C:nucleoplasm; ISS.
DR   GO; GO:0017163; F:negative regulator of basal transcription a. . .; ISS.
DR   GO; GO:0005515; F:protein binding; ISS.
DR   GO; GO:0000122; P:negative regulation of transcription from P. . .; ISS.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB_MDM2.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
SQ   SEQUENCE   487 AA;  54724 MW;  34FC5CC6A18D7744 CRC64;

  Query Match             94.8%;  Score 494;  DB 2;  Length 487;
  Best Local Similarity   90.8%;  Pred. No. 1.9e-48;
  Matches   99;  Conservative    1;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||||: ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVIFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||| ||||||| | ||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQHEPSDSGTSVSEN 125


RESULT 9
MDM2_HORSE
ID   MDM2_HORSE     STANDARD;      PRT;   491 AA.
AC   P56951;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein
DE   Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Edm2).
GN   Name=MDM2;
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20218866; PubMed=10754200;
RA   Nasir L., Burr P.D., McFarlane S.T., Gault E., Thompson H.,
RA   Argyle D.J.;
RT   "Cloning, sequence analysis and expression of the cDNAs encoding the
RT   canine and equine homologues of the mouse double minute 2 (mdm2)
RT   proto-oncogene.";
RL   Cancer Lett. 152:9-13(2000).
CC   -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC       apoptosis by binding its transcriptional activation domain.
CC       Functions as a ubiquitin ligase E3, in the presence of E1 and E2,
CC       toward p53 and itself. Permits the nuclear export of p53 and
CC       targets it for proteasome-mediated proteolysis (By similarity).
CC   -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity (By
CC       similarity).
CC   -!- SUBUNIT: Binds p53, p73, ARF(P14), ribosomal protein L5 and
CC       specifically to RNA. Can interact also with retinoblastoma protein
CC       (RB), E1A-associated protein EP300 and the E2F1 transcription
CC       factor (By similarity).
CC   -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed
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CC       predominantly in the nucleoplasm (By similarity).
CC   -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its
CC       G1 arrest and apoptosis functions. It also binds p73 and E2F1.
CC       Region II contains most of a central acidic region required for
CC       interaction with ribosomal protein L5 and a putative C4-type zinc
CC       finger. The RING finger domain which coordinates two molecules of
CC       zinc interacts specifically with RNA whether or not zinc is
CC       present and mediates the hetero-oligomerization with MDM4. It is
CC       also essential for its ubiquitin ligase E3 activity toward p53 and
CC       itself (By similarity).
CC   -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.
CC   -!- SIMILARITY: Contains 1 RanBP2-type zinc finger.
CC   -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC   -!- SIMILARITY: Contains 1 SWIB domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF121140; AAF28866.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Ligase; Metal-binding; Nuclear protein; Ubl conjugation pathway; Zinc;
KW   Zinc-finger.
FT   DOMAIN       27    107       SWIB.
FT   DOMAIN      179    185       Nuclear localization signal (Potential).
FT   DOMAIN      190    202       Nuclear export signal.
FT   DOMAIN      210    304       ARF-binding.
FT   DOMAIN      210    215       Poly-Ser.
FT   DOMAIN      242    331       Region II.
FT   DOMAIN      243    301       Asp/Glu-rich (acidic).
FT   ZN_FING     299    328       RanBP2-type.
FT   ZN_FING     438    479       RING-type.
FT   DOMAIN      466    473       Nucleolar localization signal
FT                                (Potential).
SQ   SEQUENCE   491 AA;  55279 MW;  641E033D5C1DEC39 CRC64;

  Query Match             94.8%;  Score 494;  DB 1;  Length 491;
  Best Local Similarity   90.8%;  Pred. No. 2e-48;
  Matches   99;  Conservative    2;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||||: ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVIFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||| ||||||:||| ||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVSQQEPSDSGTSVSEN 125


RESULT 10
Q7YRZ8
ID   Q7YRZ8      PRELIMINARY;      PRT;   491 AA.
AC   Q7YRZ8;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Double minute 2 protein MDM2.
GN   Name=mdm2;
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Miki R., Okuda M., Ma Z., Inokuma H., Onishi T.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB099709; BAC78209.1; -.
DR   GO; GO:0005730; C:nucleolus; ISS.
DR   GO; GO:0005654; C:nucleoplasm; ISS.
DR   GO; GO:0017163; F:negative regulator of basal transcription a. . .; ISS.
DR   GO; GO:0005515; F:protein binding; ISS.
DR   GO; GO:0000122; P:negative regulation of transcription from P. . .; ISS.
DR   InterPro; IPR003121; SWIB_MDM2.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
SQ   SEQUENCE   491 AA;  55433 MW;  D93E25D638E88934 CRC64;

  Query Match             94.2%;  Score 491;  DB 2;  Length 491;
  Best Local Similarity   89.9%;  Pred. No. 4.3e-48;
  Matches   98;  Conservative    2;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              ||:||||||| ||||| |||||||||||||||||||: ||||||||||||||||||||
Db         17 SQMPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVIFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||| |||||||| | ||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQHEPSDSGTSVSEN 125


RESULT 11
Q8WYJ2
ID   Q8WYJ2      PRELIMINARY;      PRT;   436 AA.
AC   Q8WYJ2;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   MDM2 protein.
GN   Name=MDM2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21248713; PubMed=11351297;
RA   Tamborini E., Della Torre G., Lavarino C., Azzarelli A.,
RA   Carpinelli P., Pierotti M.A., Pilotti S.;
RT   "Analysis of the molecular species generated by MDM2 gene
RT   amplification in liposarcomas.";
RL   Int. J. Cancer 92:790-796(2001).
DR   EMBL; AF092844; AAL40179.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   GO; GO:0005730; C:nucleolus; ISS.
DR   GO; GO:0005654; C:nucleoplasm; ISS.
DR   GO; GO:0017163; F:negative regulator of basal transcription a. . .; ISS.
DR   GO; GO:0005515; F:protein binding; ISS.
DR   GO; GO:0000122; P:negative regulation of transcription from P. . .; ISS.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB_MDM2.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
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DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
SQ   SEQUENCE   436 AA;  49248 MW;  3C8F55E98BC4203A CRC64;

  Query Match           87.5%;  Score 456;  DB 2;  Length 436;
  Best Local Similarity   87.6%;  Pred. No. 4.3e-44;
  Matches   92;  Conservative    1;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTS 105
              |||| ||||||| ||||||||||||| |||||||||| :    |
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQEENSDELS 121


RESULT 12
MDM2_MOUSE
ID   MDM2_MOUSE     STANDARD;      PRT;   489 AA.
AC   P23804; Q61040; Q64330;
DT   01-NOV-1991 (Rel. 20, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein
DE   Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein).
GN   Name=Mdm2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM MDM2-P90).
RX   MEDLINE=91224107; PubMed=2026149;
RA   Fakharzadeh S.S., Trusko S.P., George D.L.;
RT   "Tumorigenic potential associated with enhanced expression of a gene
RT   that is amplified in a mouse tumor cell line.";
RL   EMBO J. 10:1565-1569(1991).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM MDM2-P90).
RC   STRAIN=129/Sv;
RX   MEDLINE=97074674; PubMed=8917101;
RA   Jones S.N., Ansari-Lari M.A., Hancock A.R., Jones W.J., Gibbs R.A.,
RA   Donehower L.A., Bradley A.;
RT   "Genomic organization of the mouse double minute 2 gene.";
RL   Gene 175:209-213(1996).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM MDM2-P90).
RC   STRAIN=129/Sv;
RX   MEDLINE=96299630; PubMed=8660994;
RA   de Oca Luna R.M., Tabor A.D., Eberspaecher H., Hulboy D.L.,
RA   Worth L.L., Colman M.S., Finlay C.A., Lozano G.;
RT   "The organization and expression of the mdm2 gene.";
RL   Genomics 33:352-357(1996).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORMS MDM2-P90 AND MDM2-P76).
RX   MEDLINE=99175199; PubMed=10075719;
RA   Saucedo L.J., Myers C.D., Perry M.E.;
RT   "Multiple murine double minute gene 2 (MDM2) proteins are induced by
RT   ultraviolet light.";
RL   J. Biol. Chem. 274:8161-8168(1999).
RN   [5]
RP   NUCLEOLAR LOCALIZATION SIGNAL.
RX   MEDLINE=20180080; PubMed=10713175;
RA   Weber J.D., Kuo M.-L., Bothner B., DiGiammarino E.L., Kriwacki R.W.,
RA   Roussel M.F., Sherr C.J.;
RT   "Cooperative signals governing ARF-mdm2 interaction and nucleolar
RT   localization of the complex.";
RL   Mol. Cell. Biol. 20:2517-2528(2000).
RN   [6]
RP   PHOSPHORYLATION BY ATM.
RX   MEDLINE=20079591; PubMed=10611322;
RA   Khosravi R., Maya R., Gottlieb T., Oren M., Shiloh Y., Shkedy D.;
RT   "Rapid ATM-dependent phosphorylation of MDM2 precedes p53 accumulation
RT   in response to DNA damage.";
RL   Proc. Natl. Acad. Sci. U.S.A. 96:14973-14977(1999).
CC   -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC       apoptosis by binding its transcriptional activation domain.
CC       Functions as a ubiquitin ligase E3, in the presence of E1 and E2,
CC       toward p53 and itself. Permits the nuclear export of p53 and
CC       targets it for proteasome-mediated proteolysis.
CC   -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity.
CC   -!- SUBUNIT: Binds p53, p73, ARF(P14), ribosomal protein L5 and
CC       specifically to RNA. Can interact also with retinoblastoma protein
CC       (RB), E1A-associated protein EP300 and the E2F1 transcription
CC       factor.
CC   -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed
CC       predominantly in the nucleoplasm. Interaction with ARF(P14)
CC       results in the localization of both proteins to the nucleolus. The
CC       nucleolar localization signals in both ARF(P14) and MDM2 may be
CC       necessary to allow efficient nucleolar localization of both
CC       proteins.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Mdm2-p90;
CC         IsoId=P23804-1; Sequence=Displayed;
CC         Note=Isoform Mdm2-p76 can also be produced by alternative
CC         initiation at Met-50 of isoform Mdm2-p90, but is produced more
CC         efficiently by alternative splicing;
CC       Name=Mdm2-p76;
CC         IsoId=P23804-2; Sequence=VSP_003215;
CC         Note=Does not bind to p53;
CC       Event=Alternative initiation;
CC         Comment=2 isoforms, Mdm2-p90 (shown here) and Mdm2-p76, are
CC         produced by alternative initiation at Met-1 and Met-50. Isoform
CC         Mdm2-p76 is produced more efficiently by alternative splicing;
CC   -!- TISSUE SPECIFICITY: Ubiquitously expressed at low-level throughout
CC       embryo development and in adult tissues. MDM2-p90 is much more
CC       abundant than MDM2-p76 in testis, brain, heart, and kidney, but in
CC       the thymus, spleen, and intestine, the levels of the MDM2 proteins
CC       are roughly equivalent.
CC   -!- INDUCTION: By UV light.
CC   -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its
CC       G1 arrest and apoptosis functions. It also binds p73 and E2F1.
CC       Region II contains most of a central acidic region required for
CC       interaction with ribosomal protein L5 and a putative C4-type zinc
CC       finger. The RING finger domain which coordinates two molecules of
CC       zinc interacts specifically with RNA whether or not zinc is
CC       present and mediates the hetero-oligomerization with MDM4. It is
CC       also essential for its ubiquitin ligase E3 activity toward p53 and
CC       itself.
CC   -!- PTM: Phosphorylated in response to ionizing radiation in an ATM-
CC       dependent manner.
CC   -!- DISEASE: The gene for this protein is amplified in a mouse tumor
CC       cell line.
CC   -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.
CC   -!- SIMILARITY: Contains 1 RanBP2-type zinc finger.
CC   -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC   -!- SIMILARITY: Contains 1 SWIB domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X58876; CAA41684.1; -.
DR   EMBL; U40145; AAA91167.1; -.
DR   EMBL; U47944; AAB09030.1; -.
DR   EMBL; U47935; AAB09030.1; JOINED.
DR   EMBL; U47936; AAB09030.1; JOINED.
DR   EMBL; U47937; AAB09030.1; JOINED.
DR   EMBL; U47938; AAB09030.1; JOINED.
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DR   EMBL; U47939; AAB09030.1; JOINED.
DR   EMBL; U47940; AAB09030.1; JOINED.
DR   EMBL; U47941; AAB09030.1; JOINED.
DR   EMBL; U47942; AAB09030.1; JOINED.
DR   EMBL; U47943; AAB09030.1; JOINED.
DR   EMBL; U47934; AAB09031.1; -.
DR   PIR; S15349; S15349.
DR   HSSP; Q9UMT8; 1YCR.
DR   MGD; MGI:96952; Mdm2.
DR   GO; GO:0005634; C:nucleus; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0004842; F:ubiquitin-protein ligase activity; IDA.
DR   GO; GO:0030163; P:protein catabolism; IDA.
DR   GO; GO:0016567; P:protein ubiquitination; IDA.
DR   GO; GO:0007089; P:traversing start control point of mitotic c. . .; IDA.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Alternative initiation; Alternative splicing; Ligase; Metal-binding;
KW   Nuclear protein; Phosphorylation; Proto-oncogene;
KW   Ubl conjugation pathway; Zinc; Zinc-finger.
FT   CHAIN         1    489       Ubiquitin-protein ligase E3 Mdm2, isoform
FT                                Mdm2-p90.
FT   CHAIN        50    489       ubiquitin-protein ligase E3 Mdm2, isoform
FT                                Mdm2-p76.
FT   INIT_MET      50     50       For isoform Mdm2-p76.
FT   DOMAIN        27    107       SWIB.
FT   DOMAIN       176    182       Nuclear localization signal (Potential).
FT   DOMAIN       183    195       Nuclear export signal.
FT   DOMAIN       203    213       Poly-Ser.
FT   DOMAIN       208    302       ARF-binding.
FT   DOMAIN       240    329       Region II.
FT   DOMAIN       221    299       Asp/Glu-rich (acidic).
FT   ZN_FING      297    326       RanBP2-type.
FT   ZN_FING      436    477       RING-type.
FT   DOMAIN       464    471       Nucleolar localization signal
FT                                (Potential).
FT   VARSPLIC       1     49       Missing (in isoform Mdm2-p76).
FT                                /FTId=VSP_003215.
FT   CONFLICT     203    203       S -> T (in Ref. 1).
FT   CONFLICT     419    419       D -> H (in Ref. 1).
FT   CONFLICT     486    486       S -> T (in Ref. 3).
SQ   SEQUENCE   489 AA;  54543 MW;  4ABF489E92038DF4 CRC64;

  Query Match             85.7%;  Score 446.5;  DB 1;  Length 489;
  Best Local Similarity   81.7%;  Pred. No. 6.1e-43;
  Matches   89;  Conservative    7;  Mismatches   10;  Indels    3;  Gaps    1;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||| |||||||:: |:||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQNDTYTMKEIIFYIGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| |||:||| |||||||||||| || |||| |:||   |||||:||:
Db         77 CSNDLLGDVFGVPSFSVKEHRKIYAMIYRNLVAVSQQ---DSGTSLSES 122


RESULT 13
Q91XK7
ID   Q91XK7      PRELIMINARY;      PRT;   489 AA.
AC   Q91XK7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Mus musculus adult male lung cDNA, RIKEN full-length enriched library,
DE   clone:1200011P22 product:transformed mouse 3T3 cell double minute 2,
DE   full insert sequence (Transformed mouse 3T3 cell double minute 2) (Mus
DE   musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length
DE   enriched library, clone:E430022B10 product:transformed mouse 3T3 cell
DE   double minute 2, full insert sequence).
GN   Name=Mdm2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;
RX   MEDLINE=99279253; PubMed=10349636;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;
RX   MEDLINE=21085660; PubMed=11217851;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;
RX   MEDLINE=20499374; PubMed=11042159;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;
RX   MEDLINE=20530913; PubMed=11076861;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Lung;
RA   Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA   Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA   Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA   Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA   Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA   Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA   Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA   Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA   Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA   Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Mouse;
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RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [8]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Mouse;
RA   Strausberg R.;
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
RN   [9]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NOD; TISSUE=Thymus;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK004719; BAB23502.1; -.
DR   EMBL; BC050902; AAH50902.1; -.
DR   EMBL; AK088638; BAC40470.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   MGD; MGI:96952; Mdm2.
DR   GO; GO:0005730; C:nucleolus; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0004842; F:ubiquitin-protein ligase activity; IDA.
DR   GO; GO:0030163; P:protein catabolism; IDA.
DR   GO; GO:0016567; P:protein ubiquitination; IDA.
DR   GO; GO:0007089; P:traversing start control point of mitotic c. . .; IDA.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB_MDM2.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
SQ   SEQUENCE   489 AA;  54557 MW;  4ABF489A82038DF4 CRC64;

  Query Match             85.7%;  Score 446.5;  DB 2;  Length 489;
  Best Local Similarity   81.7%;  Pred. No. 6.1e-43;
  Matches   89;  Conservative    7;  Mismatches   10;  Indels    3;  Gaps    1;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||| |||||||:: |:||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQNDTYTMKEIIFYIGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
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               |||| |||:||| |||||||||| || |||| |:|| |||||:||:
Db         77 CSNDLLGDVFGVPSFSVKEHRKIYAMIYRNLVAVSQQ---DSGTSLSES 122


RESULT 14
Q8WYJ3
ID   Q8WYJ3      PRELIMINARY;      PRT;   118 AA.
AC   Q8WYJ3;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   MDM2 protein (Fragment).
GN   Name=MDM2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21248713; PubMed=11351297;
RA   Tamborini E., Della Torre G., Lavarino C., Azzarelli A.,
RA   Carpinelli P., Pierotti M.A., Pilotti S.;
RT   "Analysis of the molecular species generated by MDM2 gene
RT   amplification in liposarcomas.";
RL   Int. J. Cancer 92:790-796(2001).
DR   EMBL; AF092843; AAL40178.1; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB_MDM2.
DR   Pfam; PF02201; SWIB; 1.
FT   NON_TER     118    118
SQ   SEQUENCE   118 AA;  13536 MW;  D7A4DBAA83D8841B CRC64;

  Query Match             82.3%;  Score 429;  DB 2;  Length 118;
  Best Local Similarity   92.5%;  Pred. No. 1.3e-41;
  Matches   86;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

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Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVV 93
              |||| ||||||| |||||||||||||| |||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVV 109


RESULT 15
MDM2_MESAU
ID   MDM2_MESAU     STANDARD;      PRT;   466 AA.
AC   Q60524;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein
DE   Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Fragment).
GN   Name=MDM2;
OS   Mesocricetus auratus (Golden hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC   Mesocricetus.
OX   NCBI_TaxID=10036;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pancreas;
RX   MEDLINE=95300112; PubMed=7780969;
RA   Chang K.W., Laconi S., Mangold K.A., Hubchak S., Scarpelli D.G.;
RT   "Multiple genetic alterations in hamster pancreatic ductal
RT   adenocarcinomas.";
RL   Cancer Res. 55:2560-2568(1995).
CC   -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC       apoptosis by binding its transcriptional activation domain.
CC       Functions as a ubiquitin ligase E3, in the presence of E1 and E2,
CC       toward p53 and itself. Permits the nuclear export of p53 and
```

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CC       targets it for proteasome-mediated proteolysis (By similarity).
CC   -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity (By
CC       similarity).
CC   -!- SUBUNIT: Binds p53, p73, ARF(P14), ribosomal protein L5 and
CC       specifically to RNA. Can interact also with retinoblastoma protein
CC       (RB), E1A-associated protein EP300 and the E2F1 transcription
CC       factor (By similarity).
CC   -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed
CC       predominantly in the nucleoplasm (By similarity).
CC   -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its
CC       G1 arrest and apoptosis functions. It also binds p73 and E2F1.
CC       Region II contains most of a central acidic region required for
CC       interaction with ribosomal protein L5 and a putative C4-type zinc
CC       finger. The RING finger domain which coordinates two molecules of
CC       zinc interacts specifically with RNA whether or not zinc is
CC       present and mediates the hetero-oligomerization with MDM4. It is
CC       also essential for its ubiquitin ligase E3 activity toward p53 and
CC       itself (By similarity).
CC   -!- DISEASE: The gene for this protein is overexpressed in some
CC       tumors.
CC   -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.
CC   -!- SIMILARITY: Contains 1 RanBP2-type zinc finger.
CC   -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC   -!- SIMILARITY: Contains 1 SWIB domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U10982; AAC52425.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Ligase; Metal-binding; Nuclear protein; Proto-oncogene;
KW   Ubl conjugation pathway; Zinc; Zinc-finger.
FT   NON_TER       1      1
FT   DOMAIN       19     98       SWIB.
FT   DOMAIN      169    175       Nuclear localization signal (Potential).
FT   DOMAIN      176    188       Nuclear export signal.
FT   DOMAIN      196    201       Poly-Ser.
FT   DOMAIN      196    290       ARF-binding.
FT   DOMAIN      228    317       Region II.
FT   DOMAIN      209    287       Asp/Glu-rich (acidic).
FT   ZN_FING     285    314       RanBP2-type.
FT   ZN_FING     419    460       RING-type.
FT   DOMAIN      447    454       Nucleolar localization signal
FT                                (Potential).
FT   NON_TER     466    466
SQ   SEQUENCE   466 AA;  52390 MW;  78A3042163C5F939 CRC64;

  Query Match             82.2%;  Score 428.5;  DB 1;  Length 466;
  Best Local Similarity   80.7%;  Pred. No. 7.1e-41;
  Matches   88;  Conservative    7;  Mismatches   13;  Indels    1;  Gaps    1;

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              |||||||||| |||||  ||||||||||||||||||::    ||||||||||||||||
Db          9 SQIPASEQETLVRPKPLFLKLLKSVGAQKDTYTMKEII-LSWQYIMTKRLYDEKQQHIVY 67

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
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Db         68 CSNDLLGDLFGVPSFSVKDHRKIHIMIYRNLVVVSQQETLQSGTSVSES 116


Search completed: January 27, 2005, 18:13:23
Job time : 84.6 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:54:26 ; Search time 22.2 Seconds
(without alignments)
325.615 Million cell updates/sec

Title: US-10-822-254-4
Perfect score: 521
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	506	97.1	188	4	US-09-603-052-4	Sequence 4, Appli
2	506	97.1	491	1	US-07-903-103-2	Sequence 2, Appli
3	506	97.1	491	1	US-08-044-619A-2	Sequence 2, Appli
4	506	97.1	491	1	US-08-283-911-2	Sequence 2, Appli
5	506	97.1	491	1	US-08-245-500A-3	Sequence 3, Appli
6	506	97.1	491	1	US-08-390-546-3	Sequence 3, Appli
7	506	97.1	491	1	US-08-390-479A-3	Sequence 3, Appli
8	506	97.1	491	1	US-08-557-393-3	Sequence 3, Appli
9	506	97.1	491	1	US-08-390-516C-3	Sequence 3, Appli
10	506	97.1	491	1	US-08-390-517A-3	Sequence 3, Appli
11	506	97.1	491	1	US-08-390-515A-3	Sequence 3, Appli
12	506	97.1	491	2	US-08-801-718-3	Sequence 3, Appli
13	506	97.1	491	3	US-09-170-159A-3	Sequence 3, Appli
14	506	97.1	491	4	US-09-480-718-44	Sequence 44, Appl
15	489.5	94.0	216	3	US-09-510-252-4	Sequence 4, Appli
16	446.5	85.7	489	1	US-07-903-103-4	Sequence 4, Appli
17	446.5	85.7	489	1	US-08-044-619A-4	Sequence 4, Appli
18	446.5	85.7	489	1	US-08-283-911-4	Sequence 4, Appli
19	446.5	85.7	489	1	US-08-245-500A-5	Sequence 5, Appli
20	446.5	85.7	489	1	US-08-390-546-5	Sequence 5, Appli
21	446.5	85.7	489	1	US-08-390-479A-5	Sequence 5, Appli
22	446.5	85.7	489	1	US-08-557-393-5	Sequence 5, Appli
23	446.5	85.7	489	1	US-08-390-516C-5	Sequence 5, Appli
24	446.5	85.7	489	1	US-08-390-517A-5	Sequence 5, Appli
25	446.5	85.7	489	1	US-08-390-515A-5	Sequence 5, Appli
26	446.5	85.7	489	2	US-08-801-718-5	Sequence 5, Appli
27	446.5	85.7	489	3	US-09-170-159A-5	Sequence 5, Appli
28	446.5	85.7	489	4	US-09-480-718-46	Sequence 46, Appl
29	166	31.9	243	4	US-09-786-702-2	Sequence 2, Appli
30	68	13.1	206	3	US-09-311-311C-22	Sequence 22, Appl
31	62.5	12.0	505	4	US-09-252-991A-29343	Sequence 29343, A
32	62	11.9	1319	2	US-08-290-731C-2	Sequence 2, Appli
33	62	11.9	1333	3	US-09-356-952-2	Sequence 2, Appli
34	62	11.9	1333	4	US-09-976-594-312	Sequence 312, App
35	62	11.9	1336	2	US-08-290-731C-6	Sequence 6, Appli
36	61.5	11.8	658	4	US-09-248-796A-17674	Sequence 17674, A
37	61	11.7	242	4	US-09-489-039A-8331	Sequence 8331, Ap
38	61	11.7	482	4	US-09-248-796A-17755	Sequence 17755, A
39	59.5	11.4	194	3	US-09-117-257-17	Sequence 17, Appl
40	59.5	11.4	194	3	US-08-945-476-17	Sequence 17, Appl
41	59.5	11.4	194	3	US-09-489-352-17	Sequence 17, Appl
42	59.5	11.4	712	4	US-09-248-796A-19645	Sequence 19645, A
43	59	11.3	781	4	US-09-486-147-3	Sequence 3, Appli
44	58.5	11.2	145	4	US-09-270-767-43660	Sequence 43660, A
45	58	11.1	793	4	US-09-107-532A-6223	Sequence 6223, Ap

ALIGNMENTS

RESULT 1
US-09-603-052-4
; Sequence 4, Application US/09603052
; Patent No. 6492116
; GENERAL INFORMATION:
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; TITLE OF INVENTION: Assay for identifying inhibitors of the interaction
; TITLE OF INVENTION: between proteins p53 and dm2
; FILE REFERENCE: MEWB26.001C1
; CURRENT APPLICATION NUMBER: US/09/603,052
; CURRENT FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: EP 95810576.9
; PRIOR FILING DATE: 1995-09-18
; PRIOR APPLICATION NUMBER: PCT/EP96/03957
; PRIOR FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-603-052-4

Query Match 97.1%; Score 506; DB 4; Length 188;
Best Local Similarity 93.6%; Pred. No. 2.9e-60;
Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy          1 SQIPASEQETXVRPKPXLLKLLKLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
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Db         17 SQIPASEQETLVRPKPLLLKLLKLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              ||||  |||||||  |||||||||||||  ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125
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RESULT 2
US-07-903-103-2
; Sequence 2, Application US/07903103
; Patent No. 5411860
; GENERAL INFORMATION:
; APPLICANT: VOGELSTEIN, BERT
; APPLICANT: KINZLER, KENNETH
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G ST., N.W.

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;       CITY:  WASHINGTON
;       STATE:  D.C.
;       COUNTRY:  USA
;       ZIP:  20001-4597
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/903,103
;       FILING DATE:  19920623
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/867.840
;       FILING DATE:  07-APR-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  KAGAN, SARAH A.
;       REGISTRATION NUMBER:  32,141
;       REFERENCE/DOCKET NUMBER:  01107.40148
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-508-9100
;       TELEFAX:  202-508-9299
;       TELEX:  197430 BBMB UT
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  491 amino acids
;       TYPE:  AMINO ACID
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-07-903-103-2

  Query Match             97.1%;  Score 506;  DB 1;  Length 491;
  Best Local Similarity   93.6%;  Pred. No. 1e-59;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

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Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
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Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 3
US-08-044-619A-2
; Sequence 2, Application US/08044619A
; Patent No. 5420263
;  GENERAL INFORMATION:
;    APPLICANT:  THE JOHNS HOPKINS UNIVERSITY
;    APPLICANT:  720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G ST., N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001-4597
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/044,619A
;      FILING DATE:  07-APR-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/903,103
;      FILING DATE:  23-JUN-1992
;      APPLICATION NUMBER:  US 07/867.840
;      FILING DATE:  07-APR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.40148
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-044-619A-2

  Query Match             97.1%;  Score 506;  DB 1;  Length 491;
  Best Local Similarity   93.6%;  Pred. No. 1e-59;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||| ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 4
US-08-283-911-2
; Sequence 2, Application US/08283911
; Patent No. 5519118
;  GENERAL INFORMATION:
;    APPLICANT:  VOGELSTEIN, BERT
;    APPLICANT:  KINZLER, KENNETH
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G ST., N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001-4597
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/283,911
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/903,103
;      FILING DATE:  23-JUN-1992
;      APPLICATION NUMBER:  US 07/867.840
;      FILING DATE:  07-APR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.40148
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-283-911-2

  Query Match             97.1%;  Score 506;  DB 1;  Length 491;
  Best Local Similarity   93.6%;  Pred. No. 1e-59;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||||| ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 5
US-08-245-500A-3
; Sequence 3, Application US/08245500A
; Patent No. 5550023
;  GENERAL INFORMATION:
;    APPLICANT:  BURRELL, MARILEE
;    APPLICANT:  HILL, DAVID E.
;    APPLICANT:  KINZLER, KENNETH W.
;    APPLICANT:  VOGELSTEIN, BERT
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/245,500A
;      FILING DATE:  07-APR-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.42798
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-245-500A-3

  Query Match             97.1%;  Score 506;  DB 1;  Length 491;
  Best Local Similarity   93.6%;  Pred. No. 1e-59;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||||| ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 6
US-08-390-546-3
; Sequence 3, Application US/08390546
; Patent No. 5606044
;  GENERAL INFORMATION:
;    APPLICANT:  BURRELL, MARILEE
;    APPLICANT:  HILL, DAVID E.
;    APPLICANT:  KINZLER, KENNETH W.
;    APPLICANT:  VOGELSTEIN, BERT
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/390,546
;      FILING DATE:  07-APR-1993
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.42798
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-390-546-3

  Query Match             97.1%;  Score 506;  DB 1;  Length 491;
  Best Local Similarity   93.6%;  Pred. No. 1e-59;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||||| ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 7
US-08-390-479A-3
; Sequence 3, Application US/08390479A
; Patent No. 5618921
;  GENERAL INFORMATION:
;    APPLICANT:  BURRELL, MARILEE
;    APPLICANT:  HILL, DAVID E.
;    APPLICANT:  KINZLER, KENNETH W.
;    APPLICANT:  VOGELSTEIN, BERT
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
```

```
;      ADDRESSEE:  BANNER & WITCOFF, LTD.
;      STREET:  1001 G STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/390,479A
;      FILING DATE:  02-FEB-1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.48992
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-390-479A-3

  Query Match             97.1%;  Score 506;  DB 1;  Length 491;
  Best Local Similarity   93.6%;  Pred. No. 1e-59;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||| ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 8
US-08-557-393-3
; Sequence 3, Application US/08557393
; Patent No. 5702903
;  GENERAL INFORMATION:
;    APPLICANT:  BURRELL, MARILEE
;    APPLICANT:  HILL, DAVID E.
;    APPLICANT:  KINZLER, KENNETH W.
;    APPLICANT:  VOGELSTEIN, BERT
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/557,393
;      FILING DATE:  13-NOV-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/245,500
;      FILING DATE:  18-MAY-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.42798
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-557-393-3

  Query Match             97.1%;  Score 506;  DB 1;  Length 491;
  Best Local Similarity   93.6%;  Pred. No. 1e-59;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||| ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 9
US-08-390-516C-3
; Sequence 3, Application US/08390516C
; Patent No. 5708136
;  GENERAL INFORMATION:
;    APPLICANT:  BURRELL, MARILEE
;    APPLICANT:  HILL, DAVID E.
;    APPLICANT:  KINZLER, KENNETH W.
;    APPLICANT:  VOGELSTEIN, BERT
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/390,516C
;      FILING DATE:  07-APR-1993
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.42798
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
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US-08-390-516C-3

  Query Match             97.1%;  Score 506;  DB 1;  Length 491;
  Best Local Similarity   93.6%;  Pred. No. 1e-59;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
                |||| ||||||| |||||||||||||| ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 10
US-08-390-517A-3
; Sequence 3, Application US/08390517A
; Patent No. 5736338
;  GENERAL INFORMATION:
;    APPLICANT:  BURRELL, MARILEE
;    APPLICANT:  HILL, DAVID E.
;    APPLICANT:  KINZLER, KENNETH W.
;    APPLICANT:  VOGELSTEIN, BERT
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/390,517A
;      FILING DATE:  07-APR-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.42798
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-390-517A-3

  Query Match             97.1%;  Score 506;  DB 1;  Length 491;
  Best Local Similarity   93.6%;  Pred. No. 1e-59;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
                |||| ||||||| |||||||||||||| ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 11
US-08-390-515A-3
; Sequence 3, Application US/08390515A
; Patent No. 5756455
;  GENERAL INFORMATION:
;    APPLICANT:  BURRELL, MARILEE
;    APPLICANT:  HILL, DAVID E.
;    APPLICANT:  KINZLER, KENNETH W.
;    APPLICANT:  VOGELSTEIN, BERT
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/390,515A
;      FILING DATE:  07-APR-1993
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.42798
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-390-515A-3

  Query Match             97.1%;  Score 506;  DB 1;  Length 491;
  Best Local Similarity   93.6%;  Pred. No. 1e-59;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
                |||| ||||||| |||||||||||||| ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 12
US-08-801-718-3
; Sequence 3, Application US/08801718
; Patent No. 5858976
;  GENERAL INFORMATION:
;    APPLICANT:  BURRELL, MARILEE
;    APPLICANT:  HILL, DAVID E.
;    APPLICANT:  KINZLER, KENNETH W.
;    APPLICANT:  VOGELSTEIN, BERT
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
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;      COUNTRY:  USA
;      ZIP:  20001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/801,718
;      FILING DATE:  14-FEB-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/390,515
;      FILING DATE:  07-APR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.42798
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-801-718-3

  Query Match             97.1%;  Score 506;  DB 2;  Length 491;
  Best Local Similarity   93.6%;  Pred. No. 1e-59;
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RESULT 13
US-09-170-159A-3
; Sequence 3, Application US/09170159A
; Patent No. 6399755
;  GENERAL INFORMATION:
;       APPLICANT: BURRELL, MARILEE
;                  HILL, DAVID E.
;                  KINZLER, KENNETH W.
;                  VOGELSTEIN, BERT
;       TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
;                           HUMAN TUMORS
;       NUMBER OF SEQUENCES: 5
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
;            STREET: 1001 G STREET, N.W.
;            CITY: WASHINGTON
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20001
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/170,159A
;            FILING DATE: 13-Oct-1998
;            CLASSIFICATION: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: KAGAN, SARAH A.
;            REGISTRATION NUMBER: 32,141
;            REFERENCE/DOCKET NUMBER: 01107.42798
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-508-9100
;            TELEFAX: 202-508-9299
;            TELEX: 197430 BBMB UT
;  INFORMATION FOR SEQ ID NO: 3:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 491 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-170-159A-3

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  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

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RESULT 14
US-09-480-718-44
; Sequence 44, Application US/09480718
; Patent No. 6407062
; GENERAL INFORMATION:
;  APPLICANT: Sherr, Charles J
;  APPLICANT: Quelle, Dawn E
;  APPLICANT: Weber, Jason D.
;  APPLICANT: Roussel, Martine F.
;  APPLICANT: Frederique, Zindy
;  TITLE OF INVENTION: ARF-19, A NOVEL REGULATOR OF THE MAMMALIAN CELL CYCLE
;  FILE REFERENCE: 1340-1-023 CIP 1
;  CURRENT APPLICATION NUMBER: US/09/480,718
;  CURRENT FILING DATE: 2000-01-07
;  EARLIER APPLICATION NUMBER: 09/129,855
;  EARLIER FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-480-718-44

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RESULT 15
US-09-510-252-4
; Sequence 4, Application US/09510252
; Patent No. 6372490
; GENERAL INFORMATION:
;  APPLICANT: Nandabalan, Krishnan
;  APPLICANT:  Yang, Meijia
;  APPLICANT:  Schulz, Vincent
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;  APPLICANT:  CuraGen Corporation
;  TITLE OF INVENTION: MDM INTERACTING PROTEIN AND METHODS OF USE THEREOF
;  FILE REFERENCE: 15966-524 MDM US
;  CURRENT APPLICATION NUMBER: US/09/510,252
;  CURRENT FILING DATE:  2000-02-22
;  PRIOR APPLICATION NUMBER: USSN 60/121,192
;  PRIOR FILING DATE: 1999-02-23
;  PRIOR APPLICATION NUMBER: USSN 60/122,643
;  PRIOR FILING DATE: 1999-03-03
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 216
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-510-252-4

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OM protein - protein search, using sw model

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Title: US-10-822-254-4
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Sequence: 1 SQIPASEQETXVRPKPXLLK.....NLVVVNQQESSDSGTSVSEN 109

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Listing first 45 summaries

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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	506	97.1	491	9	US-09-956-425-8	Sequence 8, Appli
3	506	97.1	491	10	US-09-029-327-2	Sequence 2, Appli
4	506	97.1	491	11	US-09-966-724-2	Sequence 2, Appli
5	506	97.1	491	15	US-10-422-536-137	Sequence 137, App
6	506	97.1	491	15	US-10-232-951-35	Sequence 35, Appl
7	506	97.1	491	17	US-10-685-838-1	Sequence 1, Appli
8	506	97.1	491	17	US-10-724-225-2	Sequence 2, Appli
9	506	97.1	491	17	US-10-489-802-8	Sequence 8, Appli
10	506	97.1	491	17	US-10-723-860-2236	Sequence 2236, Ap
11	489.5	94.0	216	13	US-10-057-510-4	Sequence 4, Appli
12	480.5	92.2	522	15	US-10-287-226-380	Sequence 380, App
13	480.5	92.2	522	15	US-10-287-226-382	Sequence 382, App
14	446.5	85.7	489	9	US-09-956-425-6	Sequence 6, Appli
15	446.5	85.7	489	11	US-09-966-724-4	Sequence 4, Appli
16	446.5	85.7	489	17	US-10-489-802-6	Sequence 6, Appli
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18	430	82.5	95	17	US-10-685-838-4	Sequence 4, Appli
19	426	81.8	92	17	US-10-685-838-3	Sequence 3, Appli
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21	71	13.6	472	14	US-10-369-493-16585	Sequence 16585, A
22	71	13.6	473	15	US-10-282-122A-45311	Sequence 45311, A
23	70.5	13.5	328	17	US-10-425-115-191466	Sequence 191466,
24	69.5	13.3	291	15	US-10-425-114-59572	Sequence 59572, A
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26	68	13.1	683	14	US-10-369-493-2188	Sequence 2188, Ap
27	65.5	12.6	332	15	US-10-425-114-47234	Sequence 47234, A
28	65.5	12.6	578	16	US-10-437-963-174237	Sequence 174237,
29	65	12.5	312	15	US-10-282-122A-46159	Sequence 46159, A
30	65	12.5	757	16	US-10-437-963-156834	Sequence 156834,
31	64.5	12.4	467	14	US-10-362-774-3	Sequence 3, Appli
32	64.5	12.4	467	14	US-10-369-493-6071	Sequence 6071, Ap
33	64	12.3	413	14	US-10-369-493-17318	Sequence 17318, A
34	64	12.3	1448	16	US-10-437-963-138597	Sequence 138597,
35	63.5	12.2	226	17	US-10-494-087-18	Sequence 18, Appl
36	63.5	12.2	425	14	US-10-220-083-6	Sequence 6, Appli
37	63.5	12.2	506	16	US-10-437-963-161869	Sequence 161869,
38	63.5	12.2	709	15	US-10-282-122A-63455	Sequence 63455, A
39	63.5	12.2	821	16	US-10-437-963-110602	Sequence 110602,
40	63	12.1	1031	16	US-10-437-963-189155	Sequence 189155,
41	62.5	12.0	226	14	US-10-091-007-210	Sequence 210, App
42	62.5	12.0	451	14	US-10-369-493-17149	Sequence 17149, A
43	62.5	12.0	486	15	US-10-425-114-43529	Sequence 43529, A
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45	62	11.9	128	17	US-10-425-115-232489	Sequence 232489,

ALIGNMENTS

RESULT 1
US-09-888-077-1
; Sequence 1, Application US/09888077
; Patent No. US20020031818A1
; GENERAL INFORMATION:
; APPLICANT: Ronai, Ze'ev
; APPLICANT: Fuchs, Serge
; TITLE OF INVENTION: Modification of Mdm2 Activity
; FILE REFERENCE: 2420/1H195-US1
; CURRENT APPLICATION NUMBER: US/09/888,077
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,343
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-888-077-1

Query Match 97.1%; Score 506; DB 9; Length 491;
Best Local Similarity 93.6%; Pred. No. 2e-55;
Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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RESULT 2
US-09-956-425-8

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; Sequence 8, Application US/09956425
; Patent No. US20020045192A1
; GENERAL INFORMATION:
;  APPLICANT: Kriwacki, Richard
;  APPLICANT:  Bothner, Brian
;  APPLICANT:  Lewis, William
;  TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and Method of Use Thereof
;  FILE REFERENCE: 1340/1/035
;  CURRENT APPLICATION NUMBER: US/09/956,425
;  CURRENT FILING DATE:  2001-09-19
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-956-425-8

  Query Match             97.1%;  Score 506;  DB 9;  Length 491;
  Best Local Similarity   93.6%;  Pred. No. 2e-55;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
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Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
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RESULT 3
US-09-029-327-2
; Sequence 2, Application US/09029327
; Publication No. US20030060432A1
;  GENERAL INFORMATION:
;    APPLICANT:  TOCQUE, Bruno
;    APPLICANT:  WASYLYK, Bohdan
;    APPLICANT:  DUBS-POTERSZMAN,
;    APPLICANT:  Marie-Christine
;    TITLE OF INVENTION:  ANTAGONISTS OF THE ONCOGENIC ACTIVITY OF
;    TITLE OF INVENTION:  THE PROTEIN MDM2, AND USE THEREOF IN THE TREATMENT OF
;    TITLE OF INVENTION:  CANCERS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rhone-Poulenc Rorer Inc.
;      STREET:  500 Arcola Road, Mailstop 3C43
;      CITY:  Collegeville
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19426
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/029,327
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR 96/01340
;      FILING DATE:  02-SEP-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO FR95/10331
;      FILING DATE:  04-SEP-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fehlner Esq., Paul F.
;      REGISTRATION NUMBER:  35,135
;      REFERENCE/DOCKET NUMBER:  ST95050-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (610) 454-3839
;      TELEFAX:  (610) 454-3808
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-029-327-2

  Query Match             97.1%;  Score 506;  DB 10;  Length 491;
  Best Local Similarity   93.6%;  Pred. No. 2e-55;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

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RESULT 4
US-09-966-724-2
; Sequence 2, Application US/09966724
; Publication No. US20040170971A1
;  GENERAL INFORMATION:
;       APPLICANT: THE JOHNS HOPKINS UNIVERSITY
;                  720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA
;       TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
;                           HUMAN TUMORS
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
;            STREET: 1001 G ST., N.W.
;            CITY: WASHINGTON
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20001-4597
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/966,724
;            FILING DATE: 01-Oct-2001
;            CLASSIFICATION: 435
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/044,619
;            FILING DATE: 2001-10-01
;            APPLICATION NUMBER: US 07/867.840
;            FILING DATE: 07-APR-1992
;       ATTORNEY/AGENT INFORMATION:
;            NAME: KAGAN, SARAH A.
;            REGISTRATION NUMBER: 32,141
;            REFERENCE/DOCKET NUMBER: 01107.40148
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-508-9100
;            TELEFAX: 202-508-9299
;            TELEX: 197430 BBMB UT
;  INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 491 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-966-724-2

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  Best Local Similarity   93.6%;  Pred. No. 2e-55;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;
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Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||| ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 5
US-10-422-536-137
; Sequence 137, Application US/10422536
; Publication No. US20040014100A1
; GENERAL INFORMATION:
;  APPLICANT: Kinsella, Todd
;  APPLICANT:  Lorens, James
;  APPLICANT:  Pray, Todd
;  APPLICANT:  Bennett, Mark
;  TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR INHIBITING
;  TITLE OF INVENTION:  PROTEIN-PROTEIN INTERACTION
;  FILE REFERENCE: A-71433-1/AMP/CYO
;  CURRENT APPLICATION NUMBER: US/10/422,536
;  CURRENT FILING DATE:  2003-04-23
;  PRIOR APPLICATION NUMBER: US 60/187,130
;  PRIOR FILING DATE: 2000-03-06
;  PRIOR APPLICATION NUMBER: US 09/800,770
;  PRIOR FILING DATE: 2001-03-06
;  PRIOR APPLICATION NUMBER: US 10/232,758
;  PRIOR FILING DATE: 2002-08-30
;  NUMBER OF SEQ ID NOS: 168
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 137
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-422-536-137

  Query Match             97.1%;  Score 506;  DB 15;  Length 491;
  Best Local Similarity   93.6%;  Pred. No. 2e-55;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||| ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 6
US-10-232-951-35
; Sequence 35, Application US/10232951
; Publication No. US20040043386A1
; GENERAL INFORMATION:
;  APPLICANT: Pray, Todd
;  APPLICANT:  Wong, Brian
;  APPLICANT:  Bennett, Mark
;  APPLICANT:  Parlati, Francesco
;  APPLICANT:  Rigel Pharmaceuticals, Incorporated
;  TITLE OF INVENTION: Methods and Compositions for Functional Ubiquitin
;  TITLE OF INVENTION:  Assays
;  FILE REFERENCE: 021044-006800US
;  CURRENT APPLICATION NUMBER: US/10/232,951
;  CURRENT FILING DATE:  2002-08-30
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: E3 ubiquitin ligating agent mouse double minute 2
;   OTHER INFORMATION: (mdm2) homolog full length protein isoform, mouse
;   OTHER INFORMATION: p53-binding protein (MDM2) homolog, transcript
;   OTHER INFORMATION: variant MDM2, transformed 3T3 cell double minute 2,
;   OTHER INFORMATION: Mdm2 cDNA
US-10-232-951-35

  Query Match             97.1%;  Score 506;  DB 15;  Length 491;
  Best Local Similarity   93.6%;  Pred. No. 2e-55;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||| ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 7
US-10-685-838-1
; Sequence 1, Application US/10685838
; Publication No. US20040197893A1
; GENERAL INFORMATION:
;  APPLICANT: SHUBERT, CARSTEN
;  APPLICANT:  GRASBERGER, BRUCE
;  APPLICANT:  MAGUIRE, DIANE
;  APPLICANT:  DECKMAN, INGRID
;  APPLICANT:  SPURLINO, JOHN
;  TITLE OF INVENTION: HDM2-INHIBITOR COMPLEXES AND USES THEREOF
;  FILE REFERENCE: PRD-2137-USANP
;  CURRENT APPLICATION NUMBER: US/10/685,838
;  CURRENT FILING DATE:  2003-10-15
;  PRIOR APPLICATION NUMBER: 60/418,350
;  PRIOR FILING DATE: 2002-10-16
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-685-838-1

  Query Match             97.1%;  Score 506;  DB 17;  Length 491;
  Best Local Similarity   93.6%;  Pred. No. 2e-55;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||| ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 8
US-10-724-225-2
; Sequence 2, Application US/10724225
; Publication No. US20040209834A1
;  GENERAL INFORMATION:
;       APPLICANT: TOCQUE, Bruno
;                  WASYLYK, Bohdan
;                  DUBS-POTERSZMAN,
;                  Marie-Christine
;       TITLE OF INVENTION: ANTAGONISTS OF THE ONCOGENIC ACTIVITY OF
;                           THE PROTEIN MDM2, AND USE THEREOF IN THE TREATMENT OF
;                           CANCERS
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Rhone-Poulenc Rorer Inc.
;            STREET: 500 Arcola Road, Mailstop 3C43
;            CITY: Collegeville
```

; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/724,225
; FILING DATE: 01-Dec-2003
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/029,327
; FILING DATE: <Unknown>
; APPLICATION NUMBER: FR 96/01340
; FILING DATE: 02-SEP-1996
; APPLICATION NUMBER: WO FR95/10331
; FILING DATE: 04-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fehlner Esq., Paul F.
; REGISTRATION NUMBER: 35,135
; REFERENCE/DOCKET NUMBER: ST95050-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-724-225-2

Query Match 97.1%; Score 506; DB 17; Length 491;
Best Local Similarity 93.6%; Pred. No. 2e-55;
Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||| ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125
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RESULT 9
US-10-489-802-8
; Sequence 8, Application US/10489802
; Publication No. US20040248198A1
; GENERAL INFORMATION:
; APPLICANT: St. Jude Children's Research Hospital, Inc.
; APPLICANT: Kriwacki, Richard
; APPLICANT: Bothner, Brian
; APPLICANT: Lewis, William
; TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and
; TITLE OF INVENTION: Method of Use Thereof
; FILE REFERENCE: 44158/243642
; CURRENT APPLICATION NUMBER: US/10/489,802
; CURRENT FILING DATE: 2004-03-16
; PRIOR APPLICATION NUMBER: US 09/956,425
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-489-802-8

Query Match 97.1%; Score 506; DB 17; Length 491;
Best Local Similarity 93.6%; Pred. No. 2e-55;
Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||| ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125
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RESULT 10
US-10-723-860-2236
; Sequence 2236, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2236
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-2236

Query Match 97.1%; Score 506; DB 17; Length 491;
Best Local Similarity 93.6%; Pred. No. 2e-55;
Matches 102; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||| ||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125
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RESULT 11
US-10-057-510-4
; Sequence 4, Application US/10057510
; Publication No. US20020098580A1
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Yang, Meijia
; APPLICANT: Schulz, Vincent
; APPLICANT: CuraGen Corporation
; TITLE OF INVENTION: MDM INTERACTING PROTEIN AND METHODS OF USE THEREOF
; FILE REFERENCE: 15966-524 MDM US
; CURRENT APPLICATION NUMBER: US/10/057,510
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: USSN 09/510,252
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: USSN 60/121,192
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: USSN 60/122,643
; PRIOR FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens

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US-10-057-510-4

  Query Match             94.0%;  Score 489.5;  DB 13;  Length 216;
  Best Local Similarity   92.7%;  Pred. No. 8.6e-54;
  Matches  101;  Conservative    0;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||||||||||||| || ||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYL-QYIMTKRLYDEKQQHIVY 75

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||| ||||||||||||||||||||
Db         76 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 124


RESULT 12
US-10-287-226-380
; Sequence 380, Application US/10287226
; Publication No. US20040086875A1
; GENERAL INFORMATION:
;  APPLICANT: Agee, Michele L.,
;  APPLICANT:  Alsobrook, John P.,
;  APPLICANT:  Berghs, Constance,
;  APPLICANT:  Boldog, Ference,
;  APPLICANT:  Burgess, Catherine E.,
;  APPLICANT:  Chant, John S.,
;  APPLICANT:  Chaudhuri, Amitabha,
;  APPLICANT:  DiPippo, Vincent A.,
;  APPLICANT:  Edinger, Shlomit R.,
;  APPLICANT:  Eisen, Andrew,
;  APPLICANT:  Ellerman, Karen,
;  APPLICANT:  Gangolli, Esha A.,
;  APPLICANT:  Gorman, Linda,
;  APPLICANT:  Gerlach, Valerie,
;  APPLICANT:  Ji, Weizhen,
;  APPLICANT:  Kekuda, Ramesh,
;  APPLICANT:  Khramtsov, Nikolai,
;  APPLICANT:  Li, Li,
;  APPLICANT:  Malyankar, Uriel M.,
;  APPLICANT:  MacDougall, John R.,
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Miller, Charles E.,
;  APPLICANT:  Millet, Isabelle,
;  APPLICANT:  Ooi, Chean Eng,
;  APPLICANT:  Ort, Tatiana,
;  APPLICANT:  Padigaru, Muralidhara,
;  APPLICANT:  Patturajan, Meera,
;  APPLICANT:  Rastelli, Luca,
;  APPLICANT:  Rieger, Daniel K.,
;  APPLICANT:  Rothenberg, Mark E.,
;  APPLICANT:  Shenoy, Suresh G.,
;  APPLICANT:  Spaderna, Steven K.,
;  APPLICANT:  Spytek, Kimberley A.,
;  APPLICANT:  Taupier, Jr., Raymond J.,
;  APPLICANT:  Vernet, Corine A.M.,
;  APPLICANT:  Zerhusen, Bryan D.,
;  APPLICANT:  Zhong, Mei
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-480C
;  CURRENT APPLICATION NUMBER: US/10/287,226
;  CURRENT FILING DATE:  2002-11-04
;  PRIOR APPLICATION NUMBER: 60/334,421
;  PRIOR FILING DATE: 2001-11-30
;  PRIOR APPLICATION NUMBER: 60/354,392
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: 60/360,148
;  PRIOR FILING DATE: 2002-02-27
;  PRIOR APPLICATION NUMBER: 60/364,000
;  PRIOR FILING DATE: 2002-03-13
;  PRIOR APPLICATION NUMBER: 60/404,821
;  PRIOR FILING DATE: 2002-08-20
;  PRIOR APPLICATION NUMBER: 60/334,526
;  PRIOR FILING DATE: 2001-11-30
;  PRIOR APPLICATION NUMBER: 60/354,409
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: 60/364,227
;  PRIOR FILING DATE: 2002-03-13
;  PRIOR APPLICATION NUMBER: 60/334,027
;  PRIOR FILING DATE: 2001-11-28
;  PRIOR APPLICATION NUMBER: 60/331,641
;  PRIOR FILING DATE: 2001-11-20
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 673
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 380
;   LENGTH: 522
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-287-226-380

  Query Match             92.2%;  Score 480.5;  DB 15;  Length 522;
  Best Local Similarity   72.9%;  Pred. No. 3.7e-52;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels   31;  Gaps    1;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKE---------------------- 36
              |||||||||| ||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKERWSFTMLPRLVWNSWAQGICLPRP 76

Qy         37 -------VLXYLGQYIMTKRLYDEKQQHIVXCSNDXLGDLFGVXSFSVKEHRKIYTMIXR 89
                    || |||||||||||||||||||| |||| ||||||| |||||||||||||| |
Db         77 PKVLDLQVLFYLGQYIMTKRLYDEKQQHIVYCSNDLLGDLFGVPSFSVKEHRKIYTMIYR 136

Qy         90 NLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||
Db        137 NLVVVNQQESSDSGTSVSEN 156


RESULT 13
US-10-287-226-382
; Sequence 382, Application US/10287226
; Publication No. US20040086875A1
; GENERAL INFORMATION:
;  APPLICANT: Agee, Michele L.,
;  APPLICANT:  Alsobrook, John P.,
;  APPLICANT:  Berghs, Constance,
;  APPLICANT:  Boldog, Ference,
;  APPLICANT:  Burgess, Catherine E.,
;  APPLICANT:  Chant, John S.,
;  APPLICANT:  Chaudhuri, Amitabha,
;  APPLICANT:  DiPippo, Vincent A.,
;  APPLICANT:  Edinger, Shlomit R.,
;  APPLICANT:  Eisen, Andrew,
;  APPLICANT:  Ellerman, Karen,
;  APPLICANT:  Gangolli, Esha A.,
;  APPLICANT:  Gorman, Linda,
;  APPLICANT:  Gerlach, Valerie,
;  APPLICANT:  Ji, Weizhen,
;  APPLICANT:  Kekuda, Ramesh,
;  APPLICANT:  Khramtsov, Nikolai,
;  APPLICANT:  Li, Li,
;  APPLICANT:  Malyankar, Uriel M.,
;  APPLICANT:  MacDougall, John R.,
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Miller, Charles E.,
;  APPLICANT:  Millet, Isabelle,
;  APPLICANT:  Ooi, Chean Eng,
;  APPLICANT:  Ort, Tatiana,
;  APPLICANT:  Padigaru, Muralidhara,
;  APPLICANT:  Patturajan, Meera,
;  APPLICANT:  Rastelli, Luca,
;  APPLICANT:  Rieger, Daniel K.,
;  APPLICANT:  Rothenberg, Mark E.,
;  APPLICANT:  Shenoy, Suresh G.,
;  APPLICANT:  Spaderna, Steven K.,
;  APPLICANT:  Spytek, Kimberley A.,
;  APPLICANT:  Taupier, Jr., Raymond J.,
```

```
;  APPLICANT:  Vernet, Corine A.M.,
;  APPLICANT:  Zerhusen, Bryan D.,
;  APPLICANT:  Zhong, Mei
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-480C
;  CURRENT APPLICATION NUMBER: US/10/287,226
;  CURRENT FILING DATE:  2002-11-04
;  PRIOR APPLICATION NUMBER: 60/334,421
;  PRIOR FILING DATE: 2001-11-30
;  PRIOR APPLICATION NUMBER: 60/354,392
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: 60/360,148
;  PRIOR FILING DATE: 2002-02-27
;  PRIOR APPLICATION NUMBER: 60/364,000
;  PRIOR FILING DATE: 2002-03-13
;  PRIOR APPLICATION NUMBER: 60/404,821
;  PRIOR FILING DATE: 2002-08-20
;  PRIOR APPLICATION NUMBER: 60/334,526
;  PRIOR FILING DATE: 2001-11-30
;  PRIOR APPLICATION NUMBER: 60/354,409
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: 60/364,227
;  PRIOR FILING DATE: 2002-03-13
;  PRIOR APPLICATION NUMBER: 60/334,027
;  PRIOR FILING DATE: 2001-11-28
;  PRIOR APPLICATION NUMBER: 60/331,641
;  PRIOR FILING DATE: 2001-11-20
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 673
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 382
;   LENGTH: 522
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-287-226-382

  Query Match             92.2%;  Score 480.5;  DB 15;  Length 522;
  Best Local Similarity   72.9%;  Pred. No. 3.7e-52;
  Matches  102;  Conservative    0;  Mismatches    7;  Indels   31;  Gaps    1;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKE---------------------- 36
              |||||||||| ||||| ||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKERWSFTMLPRLVWNSWAQGICLPRP 76

Qy         37 -------VLXYLGQYIMTKRLYDEKQQHIVXCSNDXLGDLFGVXSFSVKEHRKIYTMIXR 89
                   || |||||||||||||||||| |||| ||||||| |||||||||||||| |
Db         77 PKVLDLQVLFYLGQYIMTKRLYDEKQQHIVYCSNDLLGDLFGVPSFSVKEHRKIYTMIYR 136

Qy         90 NLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||
Db        137 NLVVVNQQESSDSGTSVSEN 156


RESULT 14
US-09-956-425-6
; Sequence 6, Application US/09956425
; Patent No. US20020045192A1
; GENERAL INFORMATION:
;  APPLICANT: Kriwacki, Richard
;  APPLICANT:  Bothner, Brian
;  APPLICANT:  Lewis, William
;  TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and Method of Use Thereof
;  FILE REFERENCE: 1340/1/035
;  CURRENT APPLICATION NUMBER: US/09/956,425
;  CURRENT FILING DATE:  2001-09-19
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 489
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-956-425-6

  Query Match             85.7%;  Score 446.5;  DB 9;  Length 489;
  Best Local Similarity   81.7%;  Pred. No. 7.3e-48;
  Matches   89;  Conservative    7;  Mismatches   10;  Indels    3;  Gaps    1;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
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Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQNDTYTMKEIIFYIGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
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Db         77 CSNDLLGDVFGVPSFSVKEHRKIYAMIYRNLVAVSQQ---DSGTSLSES 122


RESULT 15
US-09-966-724-4
; Sequence 4, Application US/09966724
; Publication No. US20040170971A1
;  GENERAL INFORMATION:
;       APPLICANT: THE JOHNS HOPKINS UNIVERSITY
;                  720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA
;       TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
;                           HUMAN TUMORS
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
;            STREET: 1001 G ST., N.W.
;            CITY: WASHINGTON
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20001-4597
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/966,724
;            FILING DATE: 01-Oct-2001
;            CLASSIFICATION: 435
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/044,619
;            FILING DATE: 2001-10-01
;            APPLICATION NUMBER: US 07/867.840
;            FILING DATE: 07-APR-1992
;       ATTORNEY/AGENT INFORMATION:
;            NAME: KAGAN, SARAH A.
;            REGISTRATION NUMBER: 32,141
;            REFERENCE/DOCKET NUMBER: 01107.40148
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-508-9100
;            TELEFAX: 202-508-9299
;            TELEX: 197430 BBMB UT
;  INFORMATION FOR SEQ ID NO: 4:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 489 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-966-724-4

  Query Match             85.7%;  Score 446.5;  DB 11;  Length 489;
  Best Local Similarity   81.7%;  Pred. No. 7.3e-48;
  Matches   89;  Conservative    7;  Mismatches   10;  Indels    3;  Gaps    1;

Qy          1 SQIPASEQETXVRPKPXLLKLLKSVGAQKDTYTMKEVLXYLGQYIMTKRLYDEKQQHIVX 60
              |||||||||| ||||| |||||||||| |||||||:: |:||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQNDTYTMKEIIFYIGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDXLGDLFGVXSFSVKEHRKIYTMIXRNLVVVNQQESSDSGTSVSEN 109
              |||| |||:||| |||||||||| || |||| |:||   |||||:||:
Db         77 CSNDLLGDVFGVPSFSVKEHRKIYAMIYRNLVAVSQQ---DSGTSLSES 122
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Search completed: January 27, 2005, 18:23:04
Job time : 69.4 secs

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:45:30 ; Search time 80.8 Seconds
(without alignments)
483.929 Million cell updates/sec

Title: US-10-822-254-10
Perfect score: 555
Sequence: 1 SQIPASEQETLVRPKPLLLK.....NLVVVNQQESSDSGTSVSEN 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	545	98.2	284	2	AAR75494	Aar75494 Human dou
2	545	98.2	284	2	AAR75397	Aar75397 Human dou
3	545	98.2	491	2	AAR42175	Aar42175 Human MDM
4	545	98.2	491	2	AAR76696	Aar76696 Human MDM
5	545	98.2	491	2	AAW07887	Aaw07887 Human MDM
6	545	98.2	491	2	AAW15463	Aaw15463 Human MDM
7	545	98.2	491	2	AAW13380	Aaw13380 Human MDM
8	545	98.2	491	2	AAW13600	Aaw13600 Murine do
9	545	98.2	491	2	AAW48241	Aaw48241 Human MDM
10	545	98.2	491	2	AAW57241	Aaw57241 Human MDM
11	545	98.2	491	2	AAW42879	Aaw42879 Amino aci
12	545	98.2	491	2	AAW42971	Aaw42971 Amino aci
13	545	98.2	491	2	AAW94304	Aaw94304 Human MDM
14	545	98.2	491	3	AAY96567	Aay96567 MDM2 onco
15	545	98.2	491	4	AAB48284	Aab48284 Human MDM
16	545	98.2	491	5	AAE22654	Aae22654 Human Rin
17	545	98.2	491	5	AAE22698	Aae22698 Human Rin
18	545	98.2	491	5	AAE25913	Aae25913 Human dou
19	545	98.2	491	5	AAO15376	Aao15376 Human Dm2
20	545	98.2	491	7	ADD21815	Add21815 Human mdm
21	545	98.2	491	7	ADE61562	Ade61562 Human Pro
22	545	98.2	491	8	ADL23893	Adl23893 Human E3
23	545	98.2	491	8	ADO52353	Ado52353 Human p53
24	545	98.2	491	8	ADP12593	Adp12593 Protein e
25	545	98.2	491	8	ADN71936	Adn71936 MDM2 prot
26	545	98.2	491	8	ADQ19417	Adq19417 Human sof
27	545	98.2	1171	4	AAU32421	Aau32421 Novel hum
28	528.5	95.2	216	3	AAB08846	Aab08846 A human M
29	519.5	93.6	522	7	ADJ95152	Adj95152 Novel NOV
30	519.5	93.6	522	7	ADJ95154	Adj95154 Novel NOV
31	485.5	87.5	489	2	AAR42176	Aar42176 Murine MD
32	485.5	87.5	489	2	AAR76697	Aar76697 Mouse MDM
33	485.5	87.5	489	2	AAW07888	Aaw07888 Murine MD
34	485.5	87.5	489	2	AAW15464	Aaw15464 Murine MD
35	485.5	87.5	489	2	AAW48242	Aaw48242 Mouse MDM
36	485.5	87.5	489	2	AAW57246	Aaw57246 Mouse MDM
37	485.5	87.5	489	2	AAW42997	Aaw42997 Amino aci
38	485.5	87.5	489	2	AAW42972	Aaw42972 Amino aci
39	485.5	87.5	489	2	AAW94305	Aaw94305 Mouse MDM
40	485.5	87.5	489	5	AAE25914	Aae25914 Mouse dou
41	485.5	87.5	489	5	ABB57099	Abb57099 Mouse isc
42	485.5	87.5	489	5	AAO15375	Aao15375 Mouse Dm2
43	485.5	87.5	489	7	ADD21816	Add21816 Mouse mdm
44	485.5	87.5	489	7	ADE61560	Ade61560 Rat Prote
45	347	62.5	227	2	AAR75495	Aar75495 Human dou

ALIGNMENTS

RESULT 1
AAR75494
ID AAR75494 standard; protein; 284 AA.
XX
AC AAR75494;
XX
DT 02-FEB-1996 (first entry)
XX
DE Human double minute 2 (hdm-2) antibody-binding region fragment 1.
XX
KW Human double minute gene 2; hdm-2; antibody binding region; antigen;
KW cancer; sarcoma; rhabdomyosarcoma; diagnosis; immunoassay.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1. .284
FT /note= "amino acids 1-284 of hdm-2 gene product"
XX
PN DE4339533-A1.
XX
PD 14-JUN-1995.
XX
PF 19-NOV-1993; 93DE-04339533.
XX
PR 19-NOV-1993; 93DE-04339533.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Zentgraf H, Klein R, Frey M, Martens R;
XX
DR WPI; 1995-216248/29.
DR N-PSDB; AAQ92515.
XX
PT Detection of human double minute gene 2 (hdm-2) antibodies - by
PT incubation with new hdm-2 or antibody-binding hdm-2 fragments; useful in
PT the detection of specific cancers.
XX
PS Claim 11; Fig 1; 12pp; German.
XX
CC Fragments contg. amino acids 1-284, 58-284 and 58-491 of the hdm-2 (human
CC double minute 2) gene product are claimed. The overlapping protein
CC fragments contain binding regions for hdm-2- specific antibodies and are
CC useful for identifying such antibodies in a claimed immunoassay method.
CC The presence of anti-hdm-2 antibodies is diagnostic of certain forms of
CC cancer, e.g. rhabdomyosarcoma
XX
SQ Sequence 284 AA;

```
  Query Match             98.2%;  Score 545;  DB 2;  Length 284;
  Best Local Similarity   98.2%;  Pred. No. 1.9e-62;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 2
AAR75397
ID   AAR75397 standard; protein; 284 AA.
XX
AC   AAR75397;
XX
DT   25-MAR-2003  (revised)
DT   25-JAN-1996  (first entry)
XX
DE   Human double minute 2 (hdm-2) antibody-binding region fragment 1.
XX
KW   Human double minute gene 2; hdm-2; antibody binding region; antigen;
KW   cancer; sarcoma; rhabdomyosarcoma; diagnosis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .284
FT                   /note= "amino acids 1-284 of hdm-2 gene product"
XX
PN   DE4345249-A1.
XX
PD   24-MAY-1995.
XX
PF   19-NOV-1993;   93DE-04345249.
XX
PR   19-NOV-1993;   93DE-04339533.
XX
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI   Zentgraf H,  Klein R,  Frey M,  Martens R;
XX
DR   WPI; 1995-195167/26.
DR   N-PSDB; AAQ87261.
XX
PT   New hdm-2 fragments contg. antibody binding region - used to detect
PT   specific antibodies for diagnosis of cancers, also new DNA sequences
PT   encoding them.
XX
PS   Claim 2; Fig 1; 11pp; German.
XX
CC   Fragments contg. amino acids 1-284, 58-284 and 58-491 of the hdm-2 (human
CC   double minute 2) gene product are claimed. The overlapping protein
CC   fragments contain binding regions for hdm-2- specific antibodies and are
CC   useful for identifying such antibodies. The presence of anti-hdm-2
CC   antibodies is diagnostic of certain forms of cancer, e.g.
CC   rhabdomyosarcoma. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 284 AA;

  Query Match             98.2%;  Score 545;  DB 2;  Length 284;
  Best Local Similarity   98.2%;  Pred. No. 1.9e-62;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
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Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 3
AAR42175
ID   AAR42175 standard; protein; 491 AA.
XX
AC   AAR42175;
XX
DT   25-MAR-2003  (revised)
DT   05-MAY-1994  (first entry)
XX
DE   Human MDM2.
XX
KW   p53 gene; tumour suppressor gene; regulation; cellular proliferation;
KW   cellular transformation; carcinoma; human; tumour; MDM2; inhibition;
KW   gene amplification.
XX
OS   Homo sapiens.
XX
PN   WO9320238-A2.
XX
PD   14-OCT-1993.
XX
PF   07-APR-1993;   93WO-US003199.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Burrell M,  Hill DE,  Kinzler KW,  Vogelstein B;
XX
DR   WPI; 1993-336944/42.
DR   N-PSDB; AAQ49891.
XX
PT   Diagnosing neoplasia from amplification of MDM2 gene - or elevated gene
PT   expression, also new DNA, MDM2 protein, antibodies and treatment of
PT   sarcoma by inhibiting MDM2 expression.
XX
PS   Claim 19; Fig 1; 75pp; English.
XX
CC   This sequence is encoded by the MDM2 gene. Amplification of the MDM2 gene
CC   is diagnostic of neoplasia or the potential for neoplasia. The protein
CC   encoded by this gene interacts with the product of the p53 gene. p53 is a
CC   tumour suppressor gene and encodes a protein which appears to be a member
CC   of a group of proteins which regulate normal cellular proliferation and
CC   suppression of cellular transformation. Inactivation of the p53 gene has
CC   been implicated in the formation, or progression of a wide variety of
CC   carcinoma. Polypeptides containing at least amino acids 13-41 of p53, or
CC   the DNA encoding these, may be used to inhibit the growth of tumour cells
CC   containing MDM2 gene amplification. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 491 AA;

  Query Match             98.2%;  Score 545;  DB 2;  Length 491;
  Best Local Similarity   98.2%;  Pred. No. 4e-62;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||:
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Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 4
AAR76696
ID   AAR76696 standard; protein; 491 AA.
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XX
AC   AAR76696;
XX
DT   16-OCT-2003  (revised)
DT   01-NOV-1995  (first entry)
XX
DE   Human MDM2 protein.
XX
KW   MDM2; sarcoma; diagnostic; DNA probe.
XX
OS   Homo sapiens; (cell line CaCo-2).
XX
PN   US5420263-A.
XX
PD   30-MAY-1995.
XX
PF   07-APR-1993;   93US-00044619.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Vogelstein B,  Kinzler KW;
XX
DR   WPI; 1995-206312/27.
DR   N-PSDB; AAQ94589.
XX
PT   New human MDM2 cDNA - used to develop prods. for use in the diagnosis and
PT   treatment of tumours.
XX
PS   Claim 1; Col 23-26; 34pp; English.
XX
CC   The human MDM2 gene is genetically altered (i.e. amplified) in human
CC   tumour cells. The human MDM2 protein binds to human p53 and allows the
CC   cell to escape from p53-regulated growth. Detecting that the gene has
CC   become amplified or detecting increased gene product expression (using
CC   probes, proteins, antibodies and inhibitors) allows diagnosis and therapy
CC   of cancers such as colorectal carcinoma, lung cancer and chronic
CC   myelogenous leukaemia. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ   Sequence 491 AA;

  Query Match             98.2%;  Score 545;  DB 2;  Length 491;
  Best Local Similarity   98.2%;  Pred. No. 4e-62;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              |||||||||||||||||||||||||||||||||||||:||||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 5
AAW07887
ID   AAW07887 standard; protein; 491 AA.
XX
AC   AAW07887;
XX
DT   25-MAR-2003  (revised)
DT   28-JAN-1997  (first entry)
XX
DE   Human MDM-2, involved in tumour-development.
XX
KW   p53; MDM-2; binding-inhibitor; identification; tumour; cancer; neoplasia;
KW   antibody fusion protein; therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   166. .169
FT                   /label= phosphorylation_site
FT                   /note= "potential casein kinase II phosphorylation site"
FT   Binding-site    181. .185
FT                   /label= nuclear_localisation_signal
FT   Modified-site   192. .195
FT                   /label= phosphorylation_site
FT                   /note= "potential casein kinase II phosphorylation site"
FT   Domain          223. .274
FT                   /label= acid_activation_domain
FT   Modified-site   269. .272
FT                   /label= phosphorylation_site
FT                   /note= "potential casein kinase II phosphorylation site"
FT   Modified-site   290. .293
FT                   /label= phosphorylation_site
FT                   /note= "potential casein kinase II phosphorylation site"
FT   Domain          305. .322
FT                   /label= metal_binding_site
FT   Domain          461. .478
FT                   /label= metal_binding_site
XX
PN   US5550023-A.
XX
PD   27-AUG-1996.
XX
PF   18-MAY-1994;   94US-00245500.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
PR   07-APR-1993;   93US-00044619.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Vogelstein B,  Kinzler KW;
XX
DR   WPI; 1996-401591/40.
DR   N-PSDB; AAT45151.
XX
PT   Identification of cpds. interfering with human MDM2/p53 binding - useful
PT   as therapeutic agents to treat human neoplastic cells.
XX
PS   Claim 26; Col 25-28; 36pp; English.
XX
CC   AAW07887 represents human MDM-2 derived from a human colon carcinoma cell
CC   line, CaCo-2, cDNA library. The MDM-2 protein is used in a method for
CC   identifying compounds that interfere with the binding of p53 and MDM-2.
CC   In binding the p53 protein, the MDM-2 protein releases a cell from p53-
CC   regulated growth, allowing cancers to develop. Therefore compounds
CC   identified as interfering with the binding of MDM-2 to p53 are
CC   potentially useful in the treatment of human neoplastic cells. In the
CC   method pref. one or both of the proteins is a fusion protein esp. with an
CC   antibody or antibody fragment which aids separation and identification.
CC   (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 491 AA;

  Query Match             98.2%;  Score 545;  DB 2;  Length 491;
  Best Local Similarity   98.2%;  Pred. No. 4e-62;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              |||||||||||||||||||||||||||||||||||||:||||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 6
AAW15463
ID   AAW15463 standard; protein; 491 AA.
XX
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```
AC   AAW15463;
XX
DT   25-MAR-2003  (revised)
DT   18-JUN-1997  (first entry)
XX
DE   Human MDM2.
XX
KW   Human; MDM2 protein; antibody; detection; cancer; diagnosis;
KW   p53-regulated growth.
XX
OS   Homo sapiens.
XX
PN   US5618921-A.
XX
PD   08-APR-1997.
XX
PF   17-FEB-1995;   95US-00390479.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
PR   07-APR-1993;   93US-00044619.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Vogelstein B,  Kinzler KW,  Burrell M,  Hill DE;
XX
DR   WPI; 1997-225474/20.
DR   N-PSDB; AAT66410.
XX
PT   Antibodies specific for human MDM2 protein - for diagnosis of cancer.
XX
PS   Claim 1; Col 19-24; 35pp; English.
XX
CC   This sequence represents the human MDM2 protein. Antibodies that
CC   specifically bind to human MDM2 protein may be used for detecting
CC   elevated expression of the MDM2 gene in a human tissue or body fluid
CC   sample, esp. for cancer diagnosis. The antibodies may be used to
CC   interfere with the binding of p53 to MDM2. Elevated levels of MDM2 appear
CC   to sequester p53 and allow the cell to escape from p53-regulated growth.
CC   (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 491 AA;

  Query Match             98.2%;  Score 545;  DB 2;  Length 491;
  Best Local Similarity   98.2%;  Pred. No. 4e-62;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 7
AAW13380
ID   AAW13380 standard; protein; 491 AA.
XX
AC   AAW13380;
XX
DT   25-MAR-2003  (revised)
DT   05-JUN-1997  (first entry)
XX
DE   Human MDM2 protein.
XX
KW   Human; MDM2; CaCo-2; colonic; carcinoma; probe; detection; amplification;
KW   elevation; expression; diagnosis; neoplasia; neoplastic transformation;
KW   sarcoma; colorectal; lung cancer; chronic myelogenous leukaemia.
XX
OS   Homo sapiens.
XX
PN   US5606044-A.
XX
PD   25-FEB-1997.
XX
PF   17-FEB-1995;   95US-00390546.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
PR   07-APR-1993;   93US-00044619.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Kinzler KW,  Vogelstein B,  Hill DE,  Burrell M;
XX
DR   WPI; 1997-153623/14.
DR   N-PSDB; AAT62065.
XX
PT   Detection of amplification of human MDM2 gene - useful for diagnosis of
PT   neoplasia or potential neoplastic transformation.
XX
PS   Example 1; Col 21-24; 35pp; English.
XX
CC   The present sequence is the human MDM2 protein, the cDNA for which was
CC   isolated from a human CaCo-2 colonic carcinoma cell cDNA library using a
CC   murine MDM2 cDNA probe. The MDM2 cDNA can be used as a probe to detect
CC   the amplification or elevated expression of a human MDM2 gene, which is
CC   diagnostic of neoplasia or the potential for neoplastic transformation,
CC   useful for the detection of, e.g. sarcomas, colorectal carcinoma, lung
CC   cancer and chronic myelogenous leukaemia. (Updated on 25-MAR-2003 to
CC   correct PF field.)
XX
SQ   Sequence 491 AA;

  Query Match             98.2%;  Score 545;  DB 2;  Length 491;
  Best Local Similarity   98.2%;  Pred. No. 4e-62;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 8
AAW13600
ID   AAW13600 standard; protein; 491 AA.
XX
AC   AAW13600;
XX
DT   16-JAN-1998  (first entry)
XX
DE   Murine double minute 2 protein sequence.
XX
KW   Mouse; Mdm2; murine double minute; phosphoprotein; binding; modulation;
KW   tumour suppressor; p53; oncogene; cell cycle arrest; p107; antagonist;
KW   inhibition; transcription factor; adenocarcinoma; colon; cancer; breast;
KW   lung; stomach; myeloid leukaemia; lymphoma; hyperproliferative;
KW   restenosis.
XX
OS   Mus musculus.
XX
PN   WO9709343-A2.
XX
PD   13-MAR-1997.
XX
PF   02-SEP-1996;   96WO-FR001340.
XX
PR   04-SEP-1995;   95FR-00010331.
XX
PA   (RHON ) RHONE POULENC RORER SA.
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PA   (INRM ) INST NAT SANTE & RECH MEDICALE.
XX
PI   Tocque B,  Dubs-Poterszman M,  Wasylyk B;
XX
DR   WPI; 1997-192837/17.
DR   N-PSDB; AAT61637.
XX
PT   Treating cancer with antagonist of oncogenic activity of protein Mdm2 -
PT   or nucleic acid encoding an antagonist, also viral vectors contg. this
PT   nucleic acid.
XX
PS   Claim 2; Page 26-30; 43pp; French.
XX
CC   This is the amino acid sequence of the mouse Mdm2 (murine double minute-
CC   2) protein, a 90 kD phosphoprotein which binds and modulates the activity
CC   of the tumour suppressor protein p53. It has now been shown that the mdm2
CC   protein itself has oncogenic properties, especially in a p53-null
CC   background. Mdm2 is observed to unblock cell cycle arrest in G1 caused by
CC   over-expression of the p107 protein. This is especially done by the
CC   region covering amino acid 1-134. The invention therefore relates to
CC   antagonists able to inhibit the oncogenic activity of mdm2. These include
CC   fragments of the p53 protein, especially amino acids 1-52, 1-41, 6-41, 16
CC   -25 or 18-23 (AAW13602-6), or fragments of transcription factors e.g.
CC   TFII, TBP or TAF250, which bind amino acids 1-134 of mdm2. Other
CC   inhibitors include compounds which disrupt binding to region 135-491 of
CC   mdm2, e.g. Rb, L5 or the transcription factor E2F. The antagonists are
CC   used to treat e.g. adenocarcinoma of the colon; cancer of the breast,
CC   lung or stomach; myeloid leukaemia; B cell lymphoma, or other
CC   hyperproliferative conditions such as restenosis
XX
SQ   Sequence 491 AA;

  Query Match             98.2%;  Score 545;  DB 2;  Length 491;
  Best Local Similarity   98.2%;  Pred. No. 4e-62;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 9
AAW48241
ID   AAW48241 standard; protein; 491 AA.
XX
AC   AAW48241;
XX
DT   18-JUN-1998  (first entry)
XX
DE   Human MDM2.
XX
KW   Human; MDM2; hMDM2; tumour; cancer; diagnosis; neoplastic disease;
KW   sarcoma; liposarcoma; malignant fibrous histiocytoma; osteosarcoma.
XX
OS   Homo sapiens.
XX
PN   US5736338-A.
XX
PD   07-APR-1998.
XX
PF   17-FEB-1995;   95US-00390517.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
PR   07-APR-1993;   93US-00044619.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Vogelstein B,  Kinzler KW,  Hill DE,  Burrell M;
XX
DR   WPI; 1998-239206/21.
DR   N-PSDB; AAV20549.
XX
PT   Cancer diagnosis - by determination of MDM2 protein.
XX
PS   Claim 1; Col 25-28; 35pp; English.
XX
CC   The present sequence represents human MDM2 (hMDM2) which is used in the
CC   method of the present invention. The present invention describes a method
CC   for diagnosing a neoplastic disease caused by overexpression of MDM2
CC   protein. The method comprises detecting an elevated cellular amount of
CC   this protein. The method is useful for the diagnosis of sarcoma,
CC   especially liposarcoma, malignant fibrous histiocytoma or osteosarcoma
XX
SQ   Sequence 491 AA;

  Query Match             98.2%;  Score 545;  DB 2;  Length 491;
  Best Local Similarity   98.2%;  Pred. No. 4e-62;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 10
AAW57241
ID   AAW57241 standard; protein; 491 AA.
XX
AC   AAW57241;
XX
DT   10-AUG-1998  (first entry)
XX
DE   Human MDM2 protein.
XX
KW   Human; p53; MDM2; tumour; growth inhibition; amplification;
KW   malignant fibrous histiocytoma; liposarcoma.
XX
OS   Homo sapiens.
XX
PN   US5756455-A.
XX
PD   26-MAY-1998.
XX
PF   17-FEB-1995;   95US-00390515.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
PR   07-APR-1993;   93US-00044619.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Vogelstein B,  Kinzler KW;
XX
DR   WPI; 1998-321574/28.
DR   N-PSDB; AAV28876.
XX
PT   Inhibiting growth of tumour cells having MDM2 gene amplification - with
PT   p53 protein fragment.
XX
PS   Claim 1; Col 23-28; 40pp; English.
XX
CC   A method has been developed for inhibiting the growth of tumour cells
CC   containing a human MDM2 gene amplification. The method comprises treating
CC   the tumour cells with a DNA molecule that expresses a polypeptide capable
CC   of binding to human MDM2 protein. The present sequence represents human
CC   MDM2 protein. The present invention describes three preferred
CC   polypeptides for binding human MDM2: (1) the polypeptide comprises amino
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CC   acids 1-50 of p53 (see AAW57240); (2) the polypeptide comprises amino
CC   acids 13-41 of p53 (see AAW57240) and at least none additional p53
CC   residues on the N- or C-terminal side, provided that the polypeptide
CC   lacks the homooligomerisation domain of p53; (3) the polypeptide
CC   comprises amino acids 13-41 of p53 (see AAW57241) and at least nine
CC   additional p53 residues on the N- or C-terminal side, provided that the
CC   polypeptide lacks amino acids 138-393 of p53. Some malignant fibrous
CC   histiocytomas and liposarcomas have an MDM2 gene amplification, so
CC   detection of increased expression of MDM2 gene products indicates
CC   tumourigenesis
XX
SQ   Sequence 491 AA;

  Query Match             98.2%;  Score 545;  DB 2;  Length 491;
  Best Local Similarity   98.2%;  Pred. No. 4e-62;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 11
AAW42879
ID   AAW42879 standard; protein; 491 AA.
XX
AC   AAW42879;
XX
DT   30-APR-1998  (first entry)
XX
DE   Amino acid sequence of human MDM2.
XX
KW   MDM2; tumour; diagnosis; neoplasia; DNA binding protein; p53 polypeptide;
KW   binding; tumour cell; p53-regulated growth; inhibition;
KW   anti-cancer agent.
XX
OS   Homo sapiens.
XX
PN   US5708136-A.
XX
PD   13-JAN-1998.
XX
PF   17-FEB-1995;   95US-00390516.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
PR   07-APR-1993;   93US-00044619.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Vogelstein B,  Kinzler KW,  Burrell M,  Hill DE;
XX
DR   WPI; 1998-100408/09.
XX
PT   Human MDM2 binding polypeptide - comprises fragments of p53, useful in re
PT   -establishing p53-regulated growth control in cells over-expressing MDM2.
XX
PS   Disclosure; Col 23-28; 41pp; English.
XX
CC   The present sequence represents human MDM2. The MDM2 gene is amplified in
CC   some human tumours. The amplification of this gene is diagnostic of
CC   neoplasia or its potential. It is speculated that the MDM2 protein is a
CC   potential DNA binding protein that functions in the modulation of
CC   expression of other genes and, when present in excess, inteferes with
CC   normal constraints on cell growth. A cell containing three recombinant
CC   DNA constructs was produced. These constructs encode an MDM2 protein
CC   fused to a sequence-specific DNA binding domain, a p53 polypeptide fused
CC   to a transcriptional activation domain, and a reporter gene downstream
CC   from a DNA element which is recognised by the sequence-specific DNA-
CC   binding domain. The cell is used to identify a compound which interferes
CC   with the binding of MDM2 and p53. Since MDM2 is overexpressed in tumour
CC   cells and since binding of MDM2 to p53 appears to allow tumour cells to
CC   escape from p53-regulated growth, compounds that inhibit such binding
CC   would be useful as anti-cancer agents
XX
SQ   Sequence 491 AA;

  Query Match             98.2%;  Score 545;  DB 2;  Length 491;
  Best Local Similarity   98.2%;  Pred. No. 4e-62;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 12
AAW42971
ID   AAW42971 standard; protein; 491 AA.
XX
AC   AAW42971;
XX
DT   29-APR-1998  (first entry)
XX
DE   Amino acid sequence of human MDM2.
XX
KW   MDM2; tumour; diagnosis; neoplasia; DNA binding protein; p53 polypeptide;
KW   binding; tumour cell; p53-regulated growth; inhibition;
KW   anti-cancer agent.
XX
OS   Homo sapiens.
XX
PN   US5702903-A.
XX
PD   30-DEC-1997.
XX
PF   13-NOV-1995;   95US-00557393.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
PR   07-APR-1993;   93US-00044619.
PR   18-MAY-1994;   94US-00245500.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Vogelstein B,  Kinzler KW;
XX
DR   WPI; 1998-076411/07.
DR   N-PSDB; AAV03607.
XX
PT   Cell containing reporter construct containing human MDM2 and p53 genes -
PT   for identifying compounds that interfere with binding of human MDM2 to
PT   human p53, useful as anti-cancer agents.
XX
PS   Disclosure; Coulmns 22-28; 37pp; English.
XX
CC   The present sequence represents human MDM2. The MDM2 gene is amplified in
CC   some human tumours. The amplification of this gene is diagnostic of
CC   neoplasia or its potential. It is speculated that the MDM2 protein is a
CC   potential DNA binding protein that functions in the modulation of
CC   expression of other genes and, when present in excess, inteferes with
CC   normal constraints on cell growth. A cell containing three recombinant
CC   DNA constructs was produced. These constructs encode an MDM2 protein
CC   fused to a sequence-specific DNA binding domain, a p53 polypeptide fused
CC   to a transcriptional activation domain, and a reporter gene downstream
CC   from a DNA element which is recognised by the sequence-specific DNA-
CC   binding domain. The cell is used to identify a compound which interferes
CC   with the binding of MDM2 and p53. Since MDM2 is overexpressed in tumour
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CC   cells and since binding of MDM2 to p53 appears to allow tumour cells to
CC   escape from p53-regulated growth, compounds that inhibit such binding
CC   would be useful as anti-cancer agents
XX
SQ   Sequence 491 AA;

  Query Match             98.2%;  Score 545;  DB 2;  Length 491;
  Best Local Similarity   98.2%;  Pred. No. 4e-62;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 13
AAW94304
ID   AAW94304 standard; protein; 491 AA.
XX
AC   AAW94304;
XX
DT   13-APR-1999  (first entry)
XX
DE   Human MDM2.
XX
KW   Human; MDM2; p53; tumourigenesis; growth regulation; diagnosis;
KW   malignant fibrous histocytoma; MFH; liposarcoma.
XX
OS   Homo sapiens.
XX
PN   US5858976-A.
XX
PD   12-JAN-1999.
XX
PF   14-FEB-1997;   97US-00801718.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
PR   07-APR-1993;   93US-00044619.
PR   17-FEB-1995;   95US-00390515.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Kinzler KW,  Vogelstein B;
XX
DR   WPI; 1999-152105/13.
DR   N-PSDB; AAX03947.
XX
PT   Inhibiting growth of tumour cells having MDM2 gene amplification - with
PT   MDM2-binding p53 fragment.
XX
PS   Claim 1; Col 23-28; 41pp; English.
XX
CC   The present invention describes: (1) a method for inhibiting the growth
CC   of tumour cells which contain a human MDM2 gene amplification, comprising
CC   administering to the cells a DNA molecule that expresses a polypeptide
CC   consisting of a portion of p53 i.e. amino acids 13-41 of the 64 amino
CC   acid sequence given in AAW94303, the polypeptide being capable of binding
CC   to human MDM2 (the present sequence); (2) a method as in (1) where the
CC   polypeptide lacks the homo-oligomerisation domain of p53; and (3) a
CC   method as in (1) where the polypeptide lacks amino acids 138-393 of p53.
CC   The method is useful for treating the following tumour types which have a
CC   MDM2 gene amplification: M-7 malignant fibrous histocytoma (MFH), M-20
CC   MFH, L-9 liposarcoma, KL7 liposarcoma, KL28 liposarcoma, KL30
CC   liposarcoma, and OSA-CL MFH
XX
SQ   Sequence 491 AA;

  Query Match             98.2%;  Score 545;  DB 2;  Length 491;
  Best Local Similarity   98.2%;  Pred. No. 4e-62;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 14
AAY96567
ID   AAY96567 standard; protein; 491 AA.
XX
AC   AAY96567;
XX
DT   12-SEP-2000  (first entry)
XX
DE   MDM2 oncoprotein.
XX
KW   hEST2; telomerase; catalytic subunit; reverse transcriptase; life-span;
KW   retinoblastoma; p53; tumour suppressor; inhibitor; arteriosclerosis;
KW   proliferation; immortal; tumour therapy; macular degeneration; activator;
KW   INK4; MDM2; oncoprotein.
XX
OS   Homo sapiens.
XX
PN   WO200031238-A2.
XX
PD   02-JUN-2000.
XX
PF   24-NOV-1999;   99WO-US027907.
XX
PR   25-NOV-1998;   98US-0109891P.
PR   17-FEB-1999;   99US-0120549P.
XX
PA   (GENE-) GENETICA INC.
XX
PI   Hannon GJ,  Beach DH;
XX
DR   WPI; 2000-400055/34.
DR   N-PSDB; AAA29389.
XX
PT   New method for increasing the proliferative capacity of cell lines
PT   comprises administering agents reversibly activating telomerase activity
PT   and reversibly inactivating Rb/INk4 and/or p53 pathways useful in
PT   treating age related diseases.
XX
PS   Claim 5; Page 120; 123pp; English.
XX
CC   The invention concerns methods and reagents for extending the life-span,
CC   e.g. the number of mitotic divisions, of a cell. The method relies on
CC   activation of a telomerase activity and inhibition of one or both of a
CC   retinoblastoma (Rb)/INK4 pathway or a p53 pathway. Phosphorylation of Rb
CC   by cyclin-dependent kinases, cdk4 and cdk6, releases the cells into the
CC   division cycle. Binding of INK4 family members, e.g. the tumour
CC   suppressor p16INK4a, inhibits kinase activity and results in growth
CC   arrest. Rb inactivators can selectively and reversibly inactivate an
CC   Rb/INK4 pathway, especially an Rb/p16INK4a pathway. The oncoprotein MDM2
CC   is a cellular inhibitor of Rb/E2F function and the p53 tumour suppressor
CC   and can also be used in the methods. Other molecules which can be used
CC   include cdk4 or cdk6 mutants. In particular, a cdk4 mutant is one which
CC   differs from at one or more of residues K22, R24, H95 and/or D97.
CC   Additional constructs include a papilloma virus E7 protein, or other
CC   viral oncoprotein which bypasses Rb and/or p53. Antisense constructs of
CC   the Rb and p16INK4a genes may also be used. The methods are useful for
CC   increasing the proliferative capacity of cells. The cells are
CC   subsequently of use in pharmaceutical and cosmetic preparations used to
CC   treat conditions related to (premature) ageing, e.g. macular degeneration
CC   and arteriosclerosis. The cells can also be used to replace tumour cell
CC   lines in vitro and for studies on biochemical and physiological aspects
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CC   of growth and differentiation. Long lived (immortal) cells could also be
CC   of use in the production of normal or genetically engineered
CC   biotechnology products
XX
SQ   Sequence 491 AA;

  Query Match             98.2%;  Score 545;  DB 3;  Length 491;
  Best Local Similarity   98.2%;  Pred. No. 4e-62;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 15
AAB48284
ID   AAB48284 standard; protein; 491 AA.
XX
AC   AAB48284;
XX
DT   02-APR-2001  (first entry)
XX
DE   Human MDM2 protein.
XX
KW   S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF;
KW   CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;
KW   Bad; Bcl-2; tumour; cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO200075184-A1.
XX
PD   14-DEC-2000.
XX
PF   05-JUN-2000; 2000WO-US015449.
XX
PR   04-JUN-1999;   99US-0137494P.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Zhang H,  Tsvetkov LM,  Kondo T;
XX
DR   WPI; 2001-061703/07.
DR   N-PSDB; AAC84596.
XX
PT   Modulating polypeptide levels in a cell, diagnosing and treating tumor,
PT   involves altering levels of proteins such as S-phase kinase associated
PT   proteins 1, 2 and cullin/CDC53 proteins.
XX
PS   Claim 5; Page 93-95; 162pp; English.
XX
CC   The invention relates to methods of altering the polypeptide levels in a
CC   cell, using proteins selected from S-phase kinase associated proteins 1
CC   and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the
CC   cullin/ CDC53 family of proteins). The method is useful for altering the
CC   level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2
CC   polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for
CC   detecting tumours, and in monitoring tumor treatment in a mammal. Agents
CC   that modulate interactions between SKP and target proteins are useful for
CC   treating tumours
XX
SQ   Sequence 491 AA;

  Query Match             98.2%;  Score 545;  DB 4;  Length 491;
  Best Local Similarity   98.2%;  Pred. No. 4e-62;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


Search completed: January 27, 2005, 18:06:16
Job time : 81.8 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:52:56 ; Search time 19.8 Seconds
(without alignments)
529.678 Million cell updates/sec

Title: US-10-822-254-10
Perfect score: 555
Sequence: 1 SQIPASEQETLVRPKPLLLK.....NLVVVNQQESSDSGTSVSEN 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	545	98.2	491	1	S24354	p53-binding protei
2	485.5	87.5	489	2	S15349	mdm2 protein - mou
3	274.5	49.5	489	2	S71955	MDM2-like p53-bind
4	83	15.0	685	1	SXBPT4	NAD+-protein ADP-r
5	83	15.0	698	1	S31630	NAD+-protein ADP-r
6	83	15.0	698	1	S31714	NAD+-protein ADP-r
7	72.5	13.1	565	2	S52682	hypothetical prote
8	72.5	13.1	2833	2	A43360	inositol 1,4,5-tri
9	72	13.0	967	2	A64710	type III restricti
10	71.5	12.9	514	2	D85069	hypothetical prote
11	70.5	12.7	467	2	T25848	hypothetical prote
12	70.5	12.7	838	2	I45557	eyeless, long form
13	70	12.6	969	2	E71810	type III restricti
14	69.5	12.5	709	2	E64213	DNA topoisomerase
15	68	12.3	369	2	B70220	conserved hypothet
16	67.5	12.2	401	2	F90288	hypothetical prote
17	67.5	12.2	422	2	T26334	hypothetical prote
18	67	12.1	176	2	JQ1813	B19R protein - vac
19	67	12.1	181	2	S75415	probable ribosomal
20	67	12.1	206	1	XUBYMC	methylated-DNA-[pr
21	67	12.1	261	2	H71680	exodeoxyribonuclea
22	67	12.1	1145	2	S55600	single-stranded DN
23	66	11.9	908	2	C70168	DNA polymerase I (
24	66	11.9	1074	2	G96504	probable En/Spm-li
25	65.5	11.8	331	2	B84938	flagellar motor sw
26	65.5	11.8	425	2	T50184	mammalian swi/snf
27	65.5	11.8	447	2	I64002	sodium-translocati
28	65.5	11.8	517	2	S32169	hypothetical prote
29	65.5	11.8	525	2	T15185	hypothetical prote
30	65	11.7	134	2	G69382	response regulator
31	65	11.7	260	2	T28182	hypothetical prote
32	64.5	11.6	277	2	AI0589	conserved hypothet
33	64.5	11.6	339	2	A90395	conserved hypothet
34	64.5	11.6	366	2	T07827	1-aminocyclopropan
35	64.5	11.6	380	2	T32112	hypothetical prote
36	64.5	11.6	547	2	S64332	probable membrane
37	64.5	11.6	593	2	E81277	hypothetical prote
38	64.5	11.6	649	2	C81275	hypothetical prote
39	64.5	11.6	704	2	H82381	toxin secretion AT
40	64.5	11.6	1292	2	F64237	DNA-directed RNA p
41	64	11.5	286	2	B97743	exodeoxyribonuclea
42	64	11.5	346	2	G72094	ct244 hypothetical
43	64	11.5	346	2	G86528	CT244 hypothetical
44	64	11.5	346	2	B81574	conserved hypothet
45	64	11.5	488	2	T47943	1-aminocyclopropan

ALIGNMENTS

RESULT 1
S24354
p53-binding protein mdm2 - human
N;Alternate names: mdm-2 oncogene; mouse double minute 2 homolog; p53-associated phospho
N;Contains: p53-binding protein mdm2, splice form A
C;Species: Homo sapiens (man)
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C;Accession: S24354; S57338; G02026
R;Oliner, J.D.; Kinzler, K.W.; Meltzer, P.S.; George, D.L.; Vogelstein, B.
Nature 358, 80-83, 1992
A;Title: Amplification of a gene encoding a p53-associated protein in human sarcomas.
A;Reference number: S24354; MUID:92310576; PMID:1614537
A;Accession: S24354
A;Molecule type: mRNA
A;Residues: 1-491 <OLI>
A;Cross-references: EMBL:Z12020; NID:g35211; PIDN:CAA78055.1; PID:g35212
R;Zauberman, A.; Flusberg, D.; Haupt, Y.; Barak, Y.; Oren, M.
Nucleic Acids Res. 23, 2584-2592, 1995
A;Title: A functional p53-responsive intronic promoter is contained within the human mdm
A;Reference number: S57338; MUID:95380270; PMID:7651818
A;Accession: S57338
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-16,'P',18-24 <ZAU>
A;Cross-references: EMBL:U28935; NID:g904033; PIDN:AAA82237.1; PID:g904034
R;Lunec, J.
submitted to the EMBL Data Library, August 1995
A;Description: Multiple alternate spliced mdm2 transcripts with loss of p53 binding doma
A;Reference number: G09070
A;Accession: G02026
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-27,223-491 <LUN>
A;Cross-references: EMBL:U33199; NID:g992676; PIDN:AAA75514.1; PID:g992677
A;Experimental source: splice form A
C;Genetics:
A;Gene: GDB:MDM2
A;Cross-references: GDB:250456; OMIM:164785
A;Map position: 12q14.3-12q15
C;Superfamily: human p53-binding protein mdm2
C;Keywords: alternative splicing; oncogene; phosphoprotein
F;1-491/Product: p53-binding protein mdm-2 #status predicted <MAT1>
F;1-27,223-491/Product: p53-binding protein mdm-2, splice form A #status predicted <MAT2

Query Match 98.2%; Score 545; DB 1; Length 491;
Best Local Similarity 98.2%; Pred. No. 5e-48;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

```
Qy          61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125
```

RESULT 2
S15349
mdm2 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S15349
R;Fakharzadeh, S.S.; Trusko, S.P.; George, D.L.
EMBO J. 10, 1565-1569, 1991
A;Title: Tumorigenic potential associated with enhanced expression of a gene that is amp
A;Reference number: S15349; MUID:91224107; PMID:2026149
A;Accession: S15349
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-489 <FAK>
A;Cross-references: UNIPROT:P23804; EMBL:X58876; NID:g53038; PIDN:CAA41684.1; PID:g53039
C;Genetics:
A;Gene: mdm2
C;Superfamily: human p53-binding protein mdm2

```
  Query Match             87.5%;  Score 485.5;  DB 2;  Length 489;
  Best Local Similarity   86.2%;  Pred. No. 6.2e-42;
  Matches   94;  Conservative    9;  Mismatches    3;  Indels    3;  Gaps    1;

Qy           1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
               |||||||||||||||||||||||||| ||||||:::|:|||||||||||||||||||:
Db          17 SQIPASEQETLVRPKPLLLKLLKSVGAQNDTYTMKEIIFYIGQYIMTKRLYDEKQQHIVY 76

Qy          61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
               ||||||||:|||||||||||||||| ||||||| |:||   |||||:||:
Db          77 CSNDLLGDVFGVPSFSVKEHRKIYAMIYRNLVAVSQQ---DSGTSLSES 122
```

RESULT 3
S71955
MDM2-like p53-binding protein MDMX - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
C;Accession: S71955
R;Shvarts, A.; Steegenga, W.T.; Riteco, N.; van Laar, T.; Dekker, P.; Bazuine, M.; van H
EMBO J. 15, 5349-5357, 1996
A;Title: MDMX: a novel p53-binding protein with some functional properties of MDM2.
A;Reference number: S71955; MUID:97050840; PMID:8895579
A;Accession: S71955
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-489 <SHV>
A;Cross-references: UNIPROT:O35618; EMBL:AF007110; NID:g2253388; PIDN:AAB62927.1; PID:g2
C;Genetics:
A;Gene: MDMX
C;Function:
A;Description: inhibits transcription activation function of tumour suppressor protein p
C;Superfamily: human p53-binding protein mdm2

```
  Query Match             49.5%;  Score 274.5;  DB 2;  Length 489;
  Best Local Similarity   52.4%;  Pred. No. 2.5e-20;
  Matches   55;  Conservative   18;  Mismatches   21;  Indels   11;  Gaps    1;

Qy           5 ASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVHCSND 64
               :||| : ||||  |||:| : ||| : :|||||::|||||||| |:|||:::||:|:|  |
Db          20 SSEQISQVRPKLQLLKILHAAGAQGEVFTMKEVMHYLGQYIMVKQLYDQQEQHMVYCGGD 79

Qy          65 LLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
               ||||| |  |||||:   :| |: :|||           || | |
Db          80 LLGDLLGCQSFSVKDPSPLYDMLRKNLV----------TSASNN 113
```

RESULT 4
SXBPT4
NAD+-protein ADP-ribosyltransferase (EC 2.4.2.-) precursor - phage T4
C;Species: phage T4
A;Note: host Escherichia coli
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C;Accession: JU0096
R;Hilse, D.; Koch, T.; Rueger, W.
Nucleic Acids Res. 17, 6731, 1989
A;Title: Nucleotide sequence of the alt gene of bacteriophage T4.
A;Reference number: JU0096; MUID:89386005; PMID:2506526
A;Accession: JU0096
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-685 <HIL>
A;Cross-references: UNIPROT:P12726
C;Comment: This enzyme catalyzes the ADP-ribosylation of one of the two alpha-subunits c
C;Genetics:
A;Gene: alt
C;Superfamily: phage T4 NAD-protein ADP-ribosyltransferase
C;Keywords: glycosyltransferase; pentosyltransferase
F;7-685/Product: NAD-protein ADP-ribosyltransferase #status predicted <MAT>

```
  Query Match             15.0%;  Score 83;  DB 1;  Length 685;
  Best Local Similarity   29.0%;  Pred. No. 1.5;
  Matches   29;  Conservative   22;  Mismatches   35;  Indels   14;  Gaps    6;

Qy          18 LLKLLKS--VGAQKDTYTMKEVLYYL---GQYIMTKRL--YDEKQQHI-VHCSNDLLGDL 69
               :|::|||   |  :    : : |      |:|:: | |  ||:|  :| :|  |  | |:
Db         111 MLRILKSKTAGQARQIQVIADRLIRSRSGGRYVLLKELWDYDKKYAYILIHRKNVSLEDI 170

Qy          70 FGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
                 |||  | :   |: : :    | :|:    |:|  |::|
Db         171 PGVPEISTELFTKVESKV--GDVYINK----DTGAQVTKN 204
```

RESULT 5
S31630
NAD+-protein ADP-ribosyltransferase (EC 2.4.2.-) precursor - phage T2
C;Species: phage T2
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S31630
R;Koch, T.; Rueger, W.
submitted to the EMBL Data Library, December 1992
A;Description: The ADP-ribosyltransferase of bacteriophages T2, T4 and T6: Sequencing of
A;Reference number: S31630
A;Accession: S31630
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-698 <KOC>
A;Cross-references: UNIPROT:Q38424; EMBL:X69893; NID:g15187; PIDN:CAA49517.1; PID:g15188
C;Superfamily: phage T4 NAD-protein ADP-ribosyltransferase
C;Keywords: glycosyltransferase; NAD; pentosyltransferase

```
  Query Match             15.0%;  Score 83;  DB 1;  Length 698;
  Best Local Similarity   29.0%;  Pred. No. 1.6;
  Matches   29;  Conservative   22;  Mismatches   35;  Indels   14;  Gaps    6;

Qy          18 LLKLLKS--VGAQKDTYTMKEVLYYL---GQYIMTKRL--YDEKQQHI-VHCSNDLLGDL 69
               :|::|||   |  :    : : |      |:|:: | |  ||:|  :| :|  |  | |:
Db         112 MLRILKSKTAGQARQIQVIADRLIRSRSGGRYVLLKELWDYDKKYAYILIHRKNVSLEDI 171

Qy          70 FGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
                 |||  | :   |: : :    | :|:    |:|  |::|
Db         172 PGVPEISTELFTKVESKV--GDVYINK----DTGAQVTKN 205
```

RESULT 6
S31714
NAD+-protein ADP-ribosyltransferase (EC 2.4.2.-) precursor - phage T6
C;Species: phage T6
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S31714
R;Koch, T.; Rueger, W.
submitted to the EMBL Data Library, December 1992

```
A;Description: The ADP-ribosyltransferase of bacteriophages T2, T4 and T6: Sequencing of
A;Reference number: S31630
A;Accession: S31714
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-698 <KOC>
A;Cross-references: UNIPROT:Q38433; EMBL:X69894; NID:g15422; PIDN:CAA49518.1; PID:g15423
C;Superfamily: phage T4 NAD-protein ADP-ribosyltransferase
C;Keywords: glycosyltransferase; NAD; pentosyltransferase

  Query Match             15.0%;  Score 83;  DB 1;  Length 698;
  Best Local Similarity   29.0%;  Pred. No. 1.6;
  Matches   29;  Conservative   22;  Mismatches   35;  Indels   14;  Gaps    6;

Qy         18 LLKLLKS--VGAQKDTYTMKEVLYYL---GQYIMTKRL--YDEKQQHI-VHCSNDLLGDL 69
              :|::|||    |  :    : : |       |:|:: | |  ||:|  :| :|  |  | |:
Db        112 MLRILKSKTAGQARQIQVIADRLIRSRSGGRYVLLKELWDYDKKYAYILIHRKNVSLEDI 171

Qy         70 FGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
                |||  | :   |: : :    | :|:    |:|  |::|
Db        172 PGVPEISTELFTKVESKV--GDVYINK----DTGAQVTKN 205


RESULT 7
S52682
hypothetical protein YDR117c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YD9727.12c
C;Species: Saccharomyces cerevisiae
C;Date: 19-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S52682
R;Murphy, L.; Shore, L.; Harris, D.
submitted to the EMBL Data Library, March 1995
A;Reference number: S52671
A;Accession: S52682
A;Molecule type: DNA
A;Residues: 1-565 <MUR>
A;Cross-references: UNIPROT:Q04600; EMBL:Z48758; NID:g747879; PID:g747891; GSPDB:GN00004
C;Genetics:
A;Gene: MIPS:YDR117c
A;Cross-references: SGD:S0002524
A;Map position: 4R

  Query Match             13.1%;  Score 72.5;  DB 2;  Length 565;
  Best Local Similarity   33.3%;  Pred. No. 14;
  Matches   25;  Conservative   11;  Mismatches   30;  Indels    9;  Gaps    3;

Qy         10 TLVRPKPLLLKLLKSVGAQKDT-YTMKEVLYYLGQYIMTKRLYDEKQQHIVHCSNDLLGD 68
              || :|  |   ||| |      | || :::   : |||  | | | | :  |   :||| |
Db        362 TLYKPFNLAKDLLKEVNLASHTYYTSQDIRSAVSQYISVKNLADTKDKGKV-IMDDLLFD 420

Qy         69 LFGVPSFSVKEHRKI 83
              :       | : :|:
Db        421 M-------VNKKKKV 428


RESULT 8
A43360
inositol 1,4,5-trisphosphate receptor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A43360
R;Yoshikawa, S.; Tanimura, T.; Miyawaki, A.; Nakamura, M.; Yuzaki, M.; Furuichi, T.; Mik
J. Biol. Chem. 267, 16613-16619, 1992
A;Title: Molecular cloning and characterization of the inositol 1,4,5-trisphosphate rece
A;Reference number: A43360; MUID:92355637; PMID:1322910
A;Accession: A43360
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-2833 <YOS>
A;Cross-references: UNIPROT:P29993; GB:D90403; NID:g217337; PIDN:BAA14399.1; PID:g217338
A;Note: sequence extracted from NCBI backbone (NCBIP:111077)
C;Genetics:
A;Gene: FlyBase:Itp-r83A
A;Cross-references: FlyBase:FBgn0010051
C;Superfamily: inositol-trisphosphate receptor
C;Keywords: transmembrane protein

  Query Match             13.1%;  Score 72.5;  DB 2;  Length 2833;
  Best Local Similarity   24.3%;  Pred. No. 94;
  Matches   26;  Conservative   25;  Mismatches   37;  Indels   19;  Gaps    4;

Qy          3 IPASEQETLVRPKPLLLKLLKSVGA----------QKDTYTMKEVLYYLGQYIMTKR 49
              : ||   ::|:|:    :||::||              :||   |||::   :::
Db       1286 VTASGPGSVVKPRKHEQRLLRNVGVHTVVLDLLQNPYDEKDDELMKELMCLAHEFLQNFC 1345

Qy         50 LYDEKQQHIVHCSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQ 96
              | ::: | ::|  | |  |||  |   : | : :  :   || : |:
Db       1346 LGNQQNQVLLH--NHL--DLFLNP--GILEAKTVCAIFKDNLALCNE 1386


RESULT 9
A64710
type III restriction enzyme R protein - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: A64710
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: A64710
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-967 <TOM>
A;Cross-references: UNIPROT:O26050; GB:AE000650; GB:AE000511; NID:g2314700; PIDN:AAD0856
C;Genetics:
A;Start codon: GTG

  Query Match             13.0%;  Score 72;  DB 2;  Length 967;
  Best Local Similarity   24.8%;  Pred. No. 30;
  Matches   26;  Conservative   21;  Mismatches   44;  Indels   14;  Gaps    3;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKR---LYDEKQQH 57
              ::|  :||| | | : | |:::       | :| |:|        |  ::    |||| :
Db        768 NEIKKNEQEGLRRLEELFLEIIYQNIKDKISYQMRETT------IKNRKNDAFYDEKGEI 821

Qy         58 IVHCSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDS 102
                  |  | : : : ||:|       :| | : |: :   |:
Db        822 REFLDGSLGADKYEIKNSSVRE-----KCLYENFMQVDSEIEKDT 861


RESULT 10
D85069
hypothetical protein AT4g05520 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: D85069
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: D85069
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-514 <STO>
A;Cross-references: UNIPROT:Q9S9W1; GB:NC_001268; NID:g7267312; PIDN:CAB81094.1; GSPDB:G
C;Genetics:
A;Gene: AT4g05520
A;Map position: 4

  Query Match             12.9%;  Score 71.5;  DB 2;  Length 514;
  Best Local Similarity   29.7%;  Pred. No. 16;
  Matches   27;  Conservative   13;  Mismatches   26;  Indels   25;  Gaps    4;
```

```
Qy          15 KPLLLKLLKSVGA-----QKDTYTMKEVLYYLGQY-----------IMTKRLYDEKQQHI 58
               :|| |||::  ||      |   | : |  |:| :           : | |::::|
Db         384 QPLFLKLMRVYGALMWSLGKVLNTPEVVRVYIGSFNDKPINEVAVGPIGKELFEKEQ--- 440

Qy          59 VHCSNDLLGDLFGVPSFSVKEHRKIYTMIYR 89
                |||| ||  ||  :    |||   : |
Db         441 ----NDLLADLMDVPKKAC--DRKINEFVKR 465
```

RESULT 11
T25848
hypothetical protein T01B11.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25848
R;Geisel, C.; Stellyes, L.
submitted to the EMBL Data Library, December 1996
A;Description: The sequence of C. elegans cosmid T01B11.
A;Reference number: Z20099
A;Accession: T25848
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-467 <GEI>
A;Cross-references: UNIPROT:P91408; EMBL:U80931; PIDN:AAB37999.1; GSPDB:GN00022; CESP:T0
A;Experimental source: strain Bristol N2; clone T01B11
C;Genetics:
A;Gene: CESP:T01B11.2
A;Map position: 4
A;Introns: 39/2; 79/1; 131/2; 156/2; 337/3; 389/2
C;Superfamily: ornithine-oxo-acid aminotransferase

  Query Match 12.7%; Score 70.5; DB 2; Length 467;
  Best Local Similarity 31.6%; Pred. No. 19;
  Matches 24; Conservative 6; Mismatches 25; Indels 21; Gaps 3;

```
Qy           1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKR-----LYDEKQ 55
               |  ||:     || |  :||       :|||   |  ::|     | |     |||||
Db          13 SSTPAAAATKDVRSKEEILK------RRKDTIGSKCQIFYSDDPFMVSRASMQYLYDEKS 66

Qy          56 ----------QHIVHC 61
                         ||: ||
Db          67 NKFLDCISNVQHVGHC 82
```

RESULT 12
I45557
eyeless, long form - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 16-Aug-2004
C;Accession: I45557
R;Quiring, R.; Walldorf, U.; Kloter, U.; Gehring, W.J.
Science 265, 785-789, 1994
A;Title: Homology of the eyeless gene of Drosophila to the Small eye gene in mice and An
A;Reference number: A54584; MUID:94323757; PMID:7914031
A;Accession: I45557
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-838 <RES>
A;Cross-references: EMBL:X79493; NID:g641809; PIDN:CAA56038.1; PID:g641810
C;Genetics:
A;Gene: FlyBase:ey
A;Cross-references: FlyBase:FBgn0005558
A;Introns: 37/1; 92/2; 152/3; 371/1; 429/1; 521/1; 639/2
C;Superfamily: homeobox homology; paired box homology
C;Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulati
F;37-161/Domain: paired box homology <PBH>
F;412-468/Domain: homeobox homology <HOX>

  Query Match 12.7%; Score 70.5; DB 2; Length 838;
  Best Local Similarity 26.0%; Pred. No. 37;
  Matches 26; Conservative 14; Mismatches 33; Indels 27; Gaps 5;

```
Qy          12 VRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQY------IMTKRLYDEKQQHIVHCSNDL 65
               :||        :::|  |      ||:  : ||      |    :  |   |  |:||
Db          99 IRP--------RAIGGSKPRVATAEVVSKISQYKRECPSIFAWEIRDRLLQENV-CTND- 148

Qy          66 LGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTS 105
                  :|| |          : |||    :|:|: ||:|
Db         149 -----NIPSVS------SINRVLRNLAAQKEQQSTGSGSS 177
```

RESULT 13
E71810
type III restriction enzyme - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: E71810
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: E71810
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-969 <ARN>
A;Cross-references: UNIPROT:Q9ZJA3; GB:AE001563; GB:AE001439; NID:g4156027; PIDN:AAD0698
A;Experimental source: strain J99
C;Genetics:
A;Gene: res_2

  Query Match 12.6%; Score 70; DB 2; Length 969;
  Best Local Similarity 22.9%; Pred. No. 49;
  Matches 24; Conservative 20; Mismatches 47; Indels 14; Gaps 3;

```
Qy           1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKR---LYDEKQQH 57
               ::|  :||| | | : | |:::      | :| |:|        |  ::    |||| :
Db         770 NEIKKNEQEGLKRLEELFLEIIYQNIKDKISYQMRETT------IKNRKNDAFYDEKGE- 822

Qy          58 IVHCSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDS 102
                 : |    |   : :|        :| | : |: :   |:
Db         823 ----IREFLDGSLGADKYEIKNSSAQEKCLYENFMQVDSEIEKDT 863
```

RESULT 14
E64213
DNA topoisomerase (EC 5.99.1.2) - Mycoplasma genitalium
N;Alternate names: type I DNA topoisomerase
C;Species: Mycoplasma genitalium
C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
C;Accession: E64213
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
, C.A.; Venter, J.C.
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200; MUID:96026346; PMID:7569993
A;Accession: E64213
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-709 <TIGR>
A;Cross-references: UNIPROT:P47368; GB:U39691; GB:L43967; NID:g1045794; PID:g1045802; TI
A;Experimental source: strain G-37
C;Genetics:
A;Genetic code: SGC3
C;Superfamily: DNA topoisomerase I
C;Keywords: isomerase

  Query Match 12.5%; Score 69.5; DB 2; Length 709;
  Best Local Similarity 23.4%; Pred. No. 38;
  Matches 22; Conservative 18; Mismatches 45; Indels 9; Gaps 2;

```
Qy          21 LLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDE-----KQQHIVHCSNDLLGDLFGVPSF 75
               ::: :  :   ||  : | : |     :|||:|     | :  :  |   :|| |
```

```
Db        431 IVRFINQKNKFYTSSKSLLFDGY----QRLYEEIKPNTKDELYIDLSKLKIGDKFSFEKI 486

Qy         76 SVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              || ||:      |    :: : | |: |   : |
Db        487 SVNEHKTNPPPRYTQASLIEELEKSNIGRPSTYN 520


RESULT 15
B70220
conserved hypothetical protein BBC01 - Lyme disease spirochete plasmid C/cp9
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: B70220
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: B70220
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-369 <KLE>
A;Cross-references: UNIPROT:O50966; GB:AE000791; NID:g3253099; PIDN:AAC66310.1; PID:g268
A;Experimental source: strain B31
C;Genetics:
A;Genome: plasmid
C;Superfamily: Lyme disease spirochete plasmid conserved hypothetical protein BBG06

  Query Match             12.3%;  Score 68;  DB 2;  Length 369;
  Best Local Similarity   25.2%;  Pred. No. 26;
  Matches   27;  Conservative   21;  Mismatches   27;  Indels   32;  Gaps    7;

Qy          6 SEQETLVRPKP-----LLLKLLKSVGAQKDTYTMKEVLYYLGQYI-----------MTK 48
              |:: || : |      :|:  |: :    : || | :|||  : :           :
Db          4 SKKNTLCQNKTQHKSIVLISTLEYINKTHNKYTQKNILYYFNENLKRNGQLPVKIKTLQN 63

Qy         49 RLYD-EKQ--------QHI-VHCSNDLLGDLFGVPSFSVKE-HRKIY 84
                ||  ||:        :|: |:|  ::   |    :|| || ::|||
Db         64 YLYKLEKEIKVTTNYHKHLGVNCGTEIYYQL----NFSKKECYQKIY 106


Search completed: January 27, 2005, 18:15:11
Job time : 20.8 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:51:46 ; Search time 84.6 Seconds
(without alignments)
741.322 Million cell updates/sec

Title: US-10-822-254-10
Perfect score: 555
Sequence: 1 SQIPASEQETLVRPKPLLLK.....NLVVVNQQESSDSGTSVSEN 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	545	98.2	166	2	Q8NDW2	Q8ndw2 homo sapien
2	545	98.2	195	2	Q96DS4	Q96ds4 homo sapien
3	545	98.2	243	2	Q8TE47	Q8te47 homo sapien
4	545	98.2	491	1	MDM2_HUMAN	Q00987 homo sapien
5	545	98.2	491	2	AAP35922	Aap35922 homo sapi
6	545	98.2	491	2	AAH67077	Aah67077 homo sapi
7	533	96.0	487	1	MDM2_CANFA	P56950 canis famil
8	533	96.0	487	2	Q9GMZ6	Q9gmz6 canis famil
9	533	96.0	491	1	MDM2_HORSE	P56951 equus cabal
10	530	95.5	491	2	Q7YRZ8	Q7yrz8 felis silve
11	495	89.2	436	2	Q8WYJ2	Q8wyj2 homo sapien
12	485.5	87.5	489	1	MDM2_MOUSE	P23804 mus musculu
13	485.5	87.5	489	2	Q91XK7	Q91xk7 m mus muscu
14	468	84.3	118	2	Q8WYJ3	Q8wyj3 homo sapien
15	463.5	83.5	466	1	MDM2_MESAU	Q60524 mesocricetu
16	418	75.3	325	2	Q9PVL2	Q9pvl2 gallus gall
17	399	71.9	173	2	Q8TE46	Q8te46 homo sapien
18	368	66.3	473	1	MDM2_XENLA	P56273 xenopus lae
19	368	66.3	473	2	Q6GMB5	Q6gmb5 xenopus lae
20	367	66.1	482	2	Q6P3Q9	Q6p3q9 xenopus tro
21	367	66.1	482	2	AAH63898	Aah63898 xenopus t
22	331	59.6	105	2	Q8NDW0	Q8ndw0 homo sapien
23	315	56.8	426	2	Q9GK41	Q9gk41 canis famil
24	295.5	53.2	445	1	MDM2_BRARE	O42354 brachydanio
25	295.5	53.2	445	2	AAM00198	Aam00198 brachydan
26	280.5	50.5	446	2	Q8WYJ1	Q8wyj1 homo sapien
27	277	49.9	491	2	Q7ZUW7	Q7zuw7 brachydanio
28	275	49.5	475	2	Q7ZYI3	Q7zyi3 xenopus lae
29	274.5	49.5	489	1	MDM4_MOUSE	O35618 mus musculu
30	271.5	48.9	489	2	Q9CYG1	Q9cyg1 m mus muscu
31	265	47.7	490	2	Q99L86	Q99186 mus musculu
32	263.5	47.5	134	2	Q6PHL8	Q6phl8 xenopus lae
33	263.5	47.5	134	2	AAH56503	Aah56503 xenopus l
34	249	44.9	153	2	Q6MZR7	Q6mzr7 homo sapien
35	249	44.9	153	2	CAE45961	Cae45961 homo sapi
36	249	44.9	490	2	AAH67299	Aah67299 homo sapi
37	247	44.5	490	1	MDM4_HUMAN	O15151 homo sapien
38	220	39.6	69	2	Q86WA4	Q86wa4 homo sapien
39	213	38.4	66	2	Q96DS3	Q96ds3 homo sapien
40	210	37.8	70	2	Q86WA3	Q86wa3 homo sapien
41	196	35.3	95	2	Q96DS1	Q96ds1 homo sapien
42	179.5	32.3	70	2	Q8NDW1	Q8ndw1 homo sapien
43	177	31.9	159	2	Q96DS0	Q96ds0 homo sapien
44	176	31.7	60	2	Q96DS5	Q96ds5 homo sapien
45	176	31.7	130	2	Q9H4C3	Q9h4c3 homo sapien

ALIGNMENTS

RESULT 1
Q8NDW2
ID Q8NDW2 PRELIMINARY; PRT; 166 AA.
AC Q8NDW2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE P53-binding protein.
GN Name=MDM2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bartel F., Pinkert D., Kappler M., Bache M., Schmidt H., Taubert H.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ491698; CAD36959.1; -.
DR HSSP; Q9UMT8; 1YCR.
DR GO; GO:0005634; C:nucleus; IEA.
DR InterPro; IPR010984; MDM2.
DR InterPro; IPR003121; SWIB_MDM2.
DR Pfam; PF02201; SWIB; 1.
SQ SEQUENCE 166 AA; 18900 MW; FA6B5BA18E85040D CRC64;

Query Match 98.2%; Score 545; DB 2; Length 166;
Best Local Similarity 98.2%; Pred. No. 4.5e-50;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125
```

RESULT 2
Q96DS4
ID Q96DS4 PRELIMINARY; PRT; 195 AA.
AC Q96DS4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MDM2 variant FB26.
GN Name=MDM2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Rhabdomyosarcoma tumor;

```
RA   Bartel F., Taylor A.C., Taubert H., Harris L.C.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF385323; AAL13243.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB_MDM2.
DR   Pfam; PF02201; SWIB; 1.
SQ   SEQUENCE   195 AA;  22161 MW;  4987AE567DB12D5D CRC64;

  Query Match             98.2%;  Score 545;  DB 2;  Length 195;
  Best Local Similarity   98.2%;  Pred. No. 5.4e-50;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 3
Q8TE47
ID   Q8TE47      PRELIMINARY;      PRT;   243 AA.
AC   Q8TE47;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   MDM2 isoform KB9 protein.
GN   Name=MDM2 isoform KB9;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymphocytes;
RA   Bartel F., Pinkert D., Kappler M., Bache M., Schmidt H., Taubert H.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ430612; CAD23251.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR   GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   GO; GO:0016567; P:protein ubiquitination; IEA.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB_MDM2.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
SQ   SEQUENCE   243 AA;  27317 MW;  9EB5D0142CF185A2 CRC64;

  Query Match             98.2%;  Score 545;  DB 2;  Length 243;
  Best Local Similarity   98.2%;  Pred. No. 6.9e-50;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 4
MDM2_HUMAN
ID   MDM2_HUMAN     STANDARD;      PRT;   491 AA.
AC   Q00987; Q13226; Q13297; Q13298; Q13299; Q13300; Q13301; Q9UGI3;
AC   Q9UMT8;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein
DE   Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Hdm2).
GN   Name=MDM2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM MDM2).
RX   MEDLINE=92310576; PubMed=1614537;
RA   Oliner J.D., Kinzler K.W., Meltzer P.S., George D.L., Vogelstein B.;
RT   "Amplification of a gene encoding a p53-associated protein in human
RT   sarcomas.";
RL   Nature 358:80-83(1992).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS MDM2-A; -B; -C; -D AND -E).
RC   TISSUE=Ovarian carcinoma;
RX   MEDLINE=96313107; PubMed=8705862;
RA   Sigalas I., Calvert A.H., Anderson J.J., Neal D.E., Lunec J.;
RT   "Alternatively spliced mdm2 transcripts with loss of p53 binding
RT   domain sequences: transforming ability and frequent detection in human
RT   cancer.";
RL   Nat. Med. 2:912-917(1996).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM MDM2-ALPHA).
RX   MEDLINE=20065171; PubMed=10597303;
RA   Veldhoen N., Metcalfe S., Milner J.;
RT   "A novel exon within the mdm2 gene modulates translation initiation in
RT   vitro and disrupts the p53-binding domain of mdm2 protein.";
RL   Oncogene 18:7026-7033(1999).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM MDM2).
RA   Rieder M.J., Livingston R.J., Braun A.C., Montoya M.A., Chung M.-W.,
RA   Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA   Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RT   "NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department
RT   of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM MDM2).
RC   TISSUE=Muscle;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [6]
RP   SEQUENCE OF 6-491 FROM N.A. (ISOFORM MDM2-A1).
RA   Liang H., Atkins H., Abdel-Fattah R., Suaeyun R., Lunec J.;
RT   "Genomic organisation of the human MDM2 oncogene and relationship to
RT   its alternatively spliced mRNA's.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
RN   [7]
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RP   SEQUENCE OF 1-24 FROM N.A.
RX   MEDLINE=95380270; PubMed=7651818;
RA   Zauberman A., Flusberg D., Haupt Y., Barak Y., Oren M.;
RT   "A functional p53-responsive intronic promoter is contained within the
RT   human mdm2 gene.";
RL   Nucleic Acids Res. 23:2584-2592(1995).
RN   [8]
RP   SEQUENCE OF 1-9 FROM N.A.
RX   MEDLINE=97413643; PubMed=9270029;
RA   Landers J.E., Cassel S.L., George D.L.;
RT   "Translational enhancement of mdm2 oncogene expression in human tumor
RT   cells containing a stabilized wild-type p53 protein.";
RL   Cancer Res. 57:3562-3568(1997).
RN   [9]
RP   SEQUENCE OF 301-481 FROM N.A.
RX   MEDLINE=20542019; PubMed=11087894;
RA   Taubert H., Kappler M., Meye A., Bartel F., Schlott T.,
RA   Lautenschlaeger C., Bache M., Schmidt H., Wuerl P.;
RT   "A MboII polymorphism in exon 11 of the human MDM2 gene occuring in
RT   normal blood donors and in soft tissue sarcoma patients: an indication
RT   for an increased cancer susceptibility?";
RL   Mutat. Res. 456:39-44(2000).
RN   [10]
RP   MUTAGENESIS OF CYS-464.
RX   MEDLINE=98111004; PubMed=9450543;
RA   Honda R., Tanaka H., Yasuda H.;
RT   "Oncoprotein MDM2 is a ubiquitin ligase E3 for tumor suppressor p53.";
RL   FEBS Lett. 420:25-27(1997).
RN   [11]
RP   MUTAGENESIS OF CYS-449.
RX   MEDLINE=20190101; PubMed=10723139;
RA   Honda R., Yasuda H.;
RT   "Activity of MDM2, a ubiquitin ligase, toward p53 or itself is
RT   dependent on the RING finger domain of the ligase.";
RL   Oncogene 19:1473-1476(2000).
RN   [12]
RP   MUTAGENESIS.
RX   MEDLINE=20187618; PubMed=10722742;
RA   Fang S., Jensen J.P., Ludwig R.L., Vousden K.H., Weissman A.M.;
RT   "Mdm2 is a RING finger-dependent ubiquitin protein ligase for itself
RT   and p53.";
RL   J. Biol. Chem. 275:8945-8951(2000).
RN   [13]
RP   MUTAGENESIS OF CYS-441 AND CYS-478.
RX   MEDLINE=20076498; PubMed=10608892;
RA   Sharp D.A., Kratowicz S.A., Sank M.J., George D.L.;
RT   "Stabilization of the MDM2 oncoprotein by interaction with the
RT   structurally related MDMX protein.";
RL   J. Biol. Chem. 274:38189-38196(1999).
RN   [14]
RP   NUCLEOLAR LOCALIZATION SIGNAL.
RX   MEDLINE=20173879; PubMed=10707090;
RA   Lohrum M.A.E., Ashcroft M., Kubbutat M.H.G., Vousden K.H.;
RT   "Identification of a cryptic nucleolar-localization signal in MDM2.";
RL   Nat. Cell Biol. 2:179-181(2000).
RN   [15]
RP   PHOSPHORYLATION BY ATM.
RX   MEDLINE=20079591; PubMed=10611322;
RA   Khosravi R., Maya R., Gottlieb T., Oren M., Shiloh Y., Shkedy D.;
RT   "Rapid ATM-dependent phosphorylation of MDM2 precedes p53 accumulation
RT   in response to DNA damage.";
RL   Proc. Natl. Acad. Sci. U.S.A. 96:14973-14977(1999).
RN   [16]
RP   X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 25-109 IN COMPLEX WITH P53.
RX   MEDLINE=97081050; PubMed=8875929;
RA   Kussie P.H., Gorina S., Marechal V., Elenbaas B., Moreau J.,
RA   Levine A.J., Pavletich N.P.;
RT   "Structure of the MDM2 oncoprotein bound to the p53 tumor suppressor
RT   transactivation domain.";
RL   Science 274:948-953(1996).
CC   -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC       apoptosis by binding its transcriptional activation domain.
CC       Functions as a ubiquitin ligase E3, in the presence of E1 and E2,
CC       toward p53 and itself. Permits the nuclear export of p53 and
CC       targets it for proteasome-mediated proteolysis.
CC   -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity.
CC   -!- SUBUNIT: Binds p53, p73, ARF(P14), ribosomal protein L5 and
CC       specifically to RNA. Can interact also with retinoblastoma protein
CC       (RB), E1A-associated protein EP300 and the E2F1 transcription
CC       factor.
CC   -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed
CC       predominantly in the nucleoplasm. Interaction with ARF(P14)
CC       results in the localization of both proteins to the nucleolus. The
CC       nucleolar localization signals in both ARF(P14) and MDM2 may be
CC       necessary to allow efficient nucleolar localization of both
CC       proteins.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=8;
CC       Name=Mdm2;
CC         IsoId=Q00987-1; Sequence=Displayed;
CC       Name=Mdm2-A;
CC         IsoId=Q00987-2; Sequence=VSP_003208;
CC       Name=Mdm2-A1;
CC         IsoId=Q00987-3; Sequence=VSP_003208, VSP_003214;
CC       Name=Mdm2-B;
CC         IsoId=Q00987-4; Sequence=VSP_003209;
CC       Name=Mdm2-C;
CC         IsoId=Q00987-5; Sequence=VSP_003211;
CC       Name=Mdm2-D;
CC         IsoId=Q00987-6; Sequence=VSP_003210;
CC       Name=Mdm2-E;
CC         IsoId=Q00987-7; Sequence=VSP_003212, VSP_003213;
CC       Name=Mdm2-alpha;
CC         IsoId=Q00987-8; Sequence=VSP_003207;
CC   -!- TISSUE SPECIFICITY: Ubiquitous. Isoforms MDM2-A, -B, -C, -D and -E
CC       are observed in a range of human cancers but absent in normal
CC       tissues.
CC   -!- INDUCTION: By DNA damage.
CC   -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its
CC       G1 arrest and apoptosis functions. It also binds p73 and E2F1.
CC       Region II contains most of a central acidic region required for
CC       interaction with ribosomal protein L5 and a putative C4-type zinc
CC       finger. The RING finger domain which coordinates two molecules of
CC       zinc interacts specifically with RNA whether or not zinc is
CC       present and mediates the hetero-oligomerization with MDM4. It is
CC       also essential for its ubiquitin ligase E3 activity toward p53 and
CC       itself.
CC   -!- PTM: Phosphorylated in response to ionizing radiation in an ATM-
CC       dependent manner.
CC   -!- DISEASE: Seems to be amplified in certain tumors (including soft
CC       tissue sarcomas, osteosarcomas and gliomas). A higher frequency of
CC       splice variants lacking p53 binding domain sequences was found in
CC       late-stage and high-grade ovarian and bladder carcinomas. Four of
CC       the splice variants show loss of p53 binding.
CC   -!- MISCELLANEOUS: MDM2 RING finger mutations that failed to

  Query Match             98.2%;  Score 545;  DB 1;  Length 491;
  Best Local Similarity   98.2%;  Pred. No. 1.6e-49;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              |||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 5
AAP35922
ID   AAP35922    PRELIMINARY;      PRT;   491 AA.
AC   AAP35922;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
```

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DE   Mdm2, transformed 3T3 cell double minute 2, p53 binding protein
DE   (Mouse).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA   Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA   Phelan M., Farmer A.;
RT   "Cloning of human full-length CDSs in BD Creator(TM) System Donor
RT   vector.";
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BT007258; AAP35922.1; -.
SQ   SEQUENCE   491 AA;  55232 MW;  F37CE163876BC983 CRC64;

  Query Match             98.2%;  Score 545;  DB 2;  Length 491;
  Best Local Similarity   98.2%;  Pred. No. 1.6e-49;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 6
AAH67077
ID   AAH67077    PRELIMINARY;      PRT;   491 AA.
AC   AAH67077;
DT   14-APR-2004 (TrEMBLrel. 27, Created)
DT   14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT   14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle;
RA   Strausberg R.;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC067077; AAH67077.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   491 AA;  55232 MW;  F37CE163876BC983 CRC64;

  Query Match             98.2%;  Score 545;  DB 2;  Length 491;
  Best Local Similarity   98.2%;  Pred. No. 1.6e-49;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 7
MDM2_CANFA
ID   MDM2_CANFA     STANDARD;      PRT;   487 AA.
AC   P56950; Q95KN5;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein
DE   Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Cdm2).
GN   Name=MDM2;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE OF 1-484 FROM N.A.
RX   MEDLINE=20218866; PubMed=10754200;
RA   Nasir L., Burr P.D., McFarlane S.T., Gault E., Thompson H.,
RA   Argyle D.J.;
RT   "Cloning, sequence analysis and expression of the cDNAs encoding the
RT   canine and equine homologues of the mouse double minute 2 (mdm2)
RT   proto-oncogene.";
RL   Cancer Lett. 152:9-13(2000).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS MDM2 AND MDM2-ALPHA).
RX   MEDLINE=20065171; PubMed=10597303;
RA   Veldhoen N., Metcalfe S., Milner J.;
RT   "A novel exon within the mdm2 gene modulates translation initiation in
RT   vitro and disrupts the p53-binding domain of mdm2 protein.";
RL   Oncogene 18:7026-7033(1999).
CC   -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC       apoptosis by binding its transcriptional activation domain.
CC       Functions as a ubiquitin ligase E3, in the presence of E1 and E2,
CC       toward p53 and itself. Permits the nuclear export of p53 and
CC       targets it for proteasome-mediated proteolysis (By similarity).
CC   -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity (By
CC       similarity).
CC   -!- SUBUNIT: Binds p53, p73, ARF(P14), ribosomal protein L5 and
CC       specifically to RNA. Can interact also with retinoblastoma protein
CC       (RB), E1A-associated protein EP300 and the E2F1 transcription
CC       factor (By similarity).
CC   -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed
CC       predominantly in the nucleoplasm (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Mdm2;
CC         IsoId=P56950-1; Sequence=Displayed;
CC       Name=Mdm2-alpha;
CC         IsoId=P56950-2; Sequence=VSP_003206;
CC   -!- TISSUE SPECIFICITY: Isoform Mdm2-alpha is present in lymphoid and
CC       testicular tissues.
CC   -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its
CC       G1 arrest and apoptosis functions. It also binds p73 and E2F1.
CC       Region II contains most of a central acidic region required for
CC       interaction with ribosomal protein L5 and a putative C4-type zinc
CC       finger. The RING finger domain which coordinates two molecules of
CC       zinc interacts specifically with RNA whether or not zinc is
CC       present and mediates the hetero-oligomerization with MDM4. It is
```

```
CC       also essential for its ubiquitin ligase E3 activity toward p53 and
CC       itself (By similarity).
CC   -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.
CC   -!- SIMILARITY: Contains 1 RanBP2-type zinc finger.
CC   -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC   -!- SIMILARITY: Contains 1 SWIB domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF100705; AAF67833.1; -.
DR   EMBL; AF322416; AAG42840.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Alternative splicing; Ligase; Metal-binding; Nuclear protein;
KW   Ubl conjugation pathway; Zinc; Zinc-finger.
FT   DOMAIN       27    107       SWIB.
FT   DOMAIN      179    185       Nuclear localization signal (Potential).
FT   DOMAIN      190    202       Nuclear export signal.
FT   DOMAIN      210    304       ARF-binding.
FT   DOMAIN      210    215       Poly-Ser.
FT   DOMAIN      242    331       Region II.
FT   DOMAIN      243    301       Asp/Glu-rich (acidic).
FT   ZN_FING     299    328       RanBP2-type.
FT   ZN_FING     434    475       RING-type.
FT   DOMAIN      462    469       Nucleolar localization signal
FT                                (Potential).
FT   VARSPLIC      1     61       Missing (in isoform Mdm2-alpha).
FT                                /FTId=VSP_003206.
FT   CONFLICT     11     11       G -> D (in Ref. 2).
FT   CONFLICT    238    239       QD -> HH (in Ref. 2).
SQ   SEQUENCE   487 AA;  54696 MW;  60CDB470A32A8E69 CRC64;

  Query Match             96.0%;  Score 533;  DB 1;  Length 487;
  Best Local Similarity   95.4%;  Pred. No. 3e-48;
  Matches  104;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||||||||||||||::||||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVIFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||| | ||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQHEPSDSGTSVSEN 125


RESULT 8
Q9GMZ6
ID   Q9GMZ6      PRELIMINARY;      PRT;   487 AA.
AC   Q9GMZ6;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   MDM2.
GN   Name=mdm2;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Setoguchi A., Tsujimoto H.;
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB031276; BAB11975.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   GO; GO:0005730; C:nucleolus; ISS.
DR   GO; GO:0005654; C:nucleoplasm; ISS.
DR   GO; GO:0017163; F:negative regulator of basal transcription a. . .; ISS.
DR   GO; GO:0005515; F:protein binding; ISS.
DR   GO; GO:0000122; P:negative regulation of transcription from P. . .; ISS.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB_MDM2.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
SQ   SEQUENCE   487 AA;  54724 MW;  34FC5CC6A18D7744 CRC64;

  Query Match             96.0%;  Score 533;  DB 2;  Length 487;
  Best Local Similarity   95.4%;  Pred. No. 3e-48;
  Matches  104;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||||||||||||||::||||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVIFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||| | ||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQHEPSDSGTSVSEN 125


RESULT 9
MDM2_HORSE
ID   MDM2_HORSE     STANDARD;      PRT;   491 AA.
AC   P56951;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein
DE   Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Edm2).
GN   Name=MDM2;
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20218866; PubMed=10754200;
RA   Nasir L., Burr P.D., McFarlane S.T., Gault E., Thompson H.,
RA   Argyle D.J.;
RT   "Cloning, sequence analysis and expression of the cDNAs encoding the
RT   canine and equine homologues of the mouse double minute 2 (mdm2)
RT   proto-oncogene.";
RL   Cancer Lett. 152:9-13(2000).
CC   -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC       apoptosis by binding its transcriptional activation domain.
CC       Functions as a ubiquitin ligase E3, in the presence of E1 and E2,
CC       toward p53 and itself. Permits the nuclear export of p53 and
CC       targets it for proteasome-mediated proteolysis (By similarity).
CC   -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity (By
CC       similarity).
CC   -!- SUBUNIT: Binds p53, p73, ARF(P14), ribosomal protein L5 and
CC       specifically to RNA. Can interact also with retinoblastoma protein
CC       (RB), E1A-associated protein EP300 and the E2F1 transcription
CC       factor (By similarity).
CC   -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed
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CC       predominantly in the nucleoplasm (By similarity).
CC   -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its
CC       G1 arrest and apoptosis functions. It also binds p73 and E2F1.
CC       Region II contains most of a central acidic region required for
CC       interaction with ribosomal protein L5 and a putative C4-type zinc
CC       finger. The RING finger domain which coordinates two molecules of
CC       zinc interacts specifically with RNA whether or not zinc is
CC       present and mediates the hetero-oligomerization with MDM4. It is
CC       also essential for its ubiquitin ligase E3 activity toward p53 and
CC       itself (By similarity).
CC   -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.
CC   -!- SIMILARITY: Contains 1 RanBP2-type zinc finger.
CC   -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC   -!- SIMILARITY: Contains 1 SWIB domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF121140; AAF28866.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Ligase; Metal-binding; Nuclear protein; Ubl conjugation pathway; Zinc;
KW   Zinc-finger.
FT   DOMAIN       27    107       SWIB.
FT   DOMAIN      179    185       Nuclear localization signal (Potential).
FT   DOMAIN      190    202       Nuclear export signal.
FT   DOMAIN      210    304       ARF-binding.
FT   DOMAIN      210    215       Poly-Ser.
FT   DOMAIN      242    331       Region II.
FT   DOMAIN      243    301       Asp/Glu-rich (acidic).
FT   ZN_FING     299    328       RanBP2-type.
FT   ZN_FING     438    479       RING-type.
FT   DOMAIN      466    473       Nucleolar localization signal
FT                                (Potential).
SQ   SEQUENCE   491 AA;  55279 MW;  641E033D5C1DEC39 CRC64;

  Query Match             96.0%;  Score 533;  DB 1;  Length 491;
  Best Local Similarity   95.4%;  Pred. No. 3e-48;
  Matches  104;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||||||||||::||||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVIFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||||||||||||:||| ||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVSQQEPSDSGTSVSEN 125


RESULT 10
Q7YRZ8
ID   Q7YRZ8      PRELIMINARY;      PRT;   491 AA.
AC   Q7YRZ8;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Double minute 2 protein MDM2.
GN   Name=mdm2;
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Miki R., Okuda M., Ma Z., Inokuma H., Onishi T.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB099709; BAC78209.1; -.
DR   GO; GO:0005730; C:nucleolus; ISS.
DR   GO; GO:0005654; C:nucleoplasm; ISS.
DR   GO; GO:0017163; F:negative regulator of basal transcription a. . .; ISS.
DR   GO; GO:0005515; F:protein binding; ISS.
DR   GO; GO:0000122; P:negative regulation of transcription from P. . .; ISS.
DR   InterPro; IPR003121; SWIB_MDM2.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
SQ   SEQUENCE   491 AA;  55433 MW;  D93E25D638E88934 CRC64;

  Query Match             95.5%;  Score 530;  DB 2;  Length 491;
  Best Local Similarity   94.5%;  Pred. No. 6.3e-48;
  Matches  103;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||:|||||||||||||||||||||||||||||||::||||||||||||||||||||:
Db         17 SQMPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVIFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||| | ||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQHEPSDSGTSVSEN 125


RESULT 11
Q8WYJ2
ID   Q8WYJ2      PRELIMINARY;      PRT;   436 AA.
AC   Q8WYJ2;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   MDM2 protein.
GN   Name=MDM2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21248713; PubMed=11351297;
RA   Tamborini E., Della Torre G., Lavarino C., Azzarelli A.,
RA   Carpinelli P., Pierotti M.A., Pilotti S.;
RT   "Analysis of the molecular species generated by MDM2 gene
RT   amplification in liposarcomas.";
RL   Int. J. Cancer 92:790-796(2001).
DR   EMBL; AF092844; AAL40179.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   GO; GO:0005730; C:nucleolus; ISS.
DR   GO; GO:0005654; C:nucleoplasm; ISS.
DR   GO; GO:0017163; F:negative regulator of basal transcription a. . .; ISS.
DR   GO; GO:0005515; F:protein binding; ISS.
DR   GO; GO:0000122; P:negative regulation of transcription from P. . .; ISS.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB_MDM2.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
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DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
SQ   SEQUENCE   436 AA;  49248 MW;  3C8F55E98BC4203A CRC64;

  Query Match          89.2%;  Score 495;  DB 2;  Length 436;
  Best Local Similarity   92.4%;  Pred. No. 3e-44;
  Matches   97;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTS 105
              |||||||||||||||||||||||||||||||||| :    |
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQEENSDELS 121


RESULT 12
MDM2_MOUSE
ID   MDM2_MOUSE     STANDARD;      PRT;   489 AA.
AC   P23804; Q61040; Q64330;
DT   01-NOV-1991 (Rel. 20, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein
DE   Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein).
GN   Name=Mdm2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM MDM2-P90).
RX   MEDLINE=91224107; PubMed=2026149;
RA   Fakharzadeh S.S., Trusko S.P., George D.L.;
RT   "Tumorigenic potential associated with enhanced expression of a gene
RT   that is amplified in a mouse tumor cell line.";
RL   EMBO J. 10:1565-1569(1991).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM MDM2-P90).
RC   STRAIN=129/Sv;
RX   MEDLINE=97074674; PubMed=8917101;
RA   Jones S.N., Ansari-Lari M.A., Hancock A.R., Jones W.J., Gibbs R.A.,
RA   Donehower L.A., Bradley A.;
RT   "Genomic organization of the mouse double minute 2 gene.";
RL   Gene 175:209-213(1996).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM MDM2-P90).
RC   STRAIN=129/Sv;
RX   MEDLINE=96299630; PubMed=8660994;
RA   de Oca Luna R.M., Tabor A.D., Eberspaecher H., Hulboy D.L.,
RA   Worth L.L., Colman M.S., Finlay C.A., Lozano G.;
RT   "The organization and expression of the mdm2 gene.";
RL   Genomics 33:352-357(1996).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORMS MDM2-P90 AND MDM2-P76).
RX   MEDLINE=99175199; PubMed=10075719;
RA   Saucedo L.J., Myers C.D., Perry M.E.;
RT   "Multiple murine double minute gene 2 (MDM2) proteins are induced by
RT   ultraviolet light.";
RL   J. Biol. Chem. 274:8161-8168(1999).
RN   [5]
RP   NUCLEOLAR LOCALIZATION SIGNAL.
RX   MEDLINE=20180080; PubMed=10713175;
RA   Weber J.D., Kuo M.-L., Bothner B., DiGiammarino E.L., Kriwacki R.W.,
RA   Roussel M.F., Sherr C.J.;
RT   "Cooperative signals governing ARF-mdm2 interaction and nucleolar
RT   localization of the complex.";
RL   Mol. Cell. Biol. 20:2517-2528(2000).
RN   [6]
RP   PHOSPHORYLATION BY ATM.
RX   MEDLINE=20079591; PubMed=10611322;
RA   Khosravi R., Maya R., Gottlieb T., Oren M., Shiloh Y., Shkedy D.;
RT   "Rapid ATM-dependent phosphorylation of MDM2 precedes p53 accumulation
RT   in response to DNA damage.";
RL   Proc. Natl. Acad. Sci. U.S.A. 96:14973-14977(1999).
CC   -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC       apoptosis by binding its transcriptional activation domain.
CC       Functions as a ubiquitin ligase E3, in the presence of E1 and E2,
CC       toward p53 and itself. Permits the nuclear export of p53 and
CC       targets it for proteasome-mediated proteolysis.
CC   -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity.
CC   -!- SUBUNIT: Binds p53, p73, ARF(P14), ribosomal protein L5 and
CC       specifically to RNA. Can interact also with retinoblastoma protein
CC       (RB), E1A-associated protein EP300 and the E2F1 transcription
CC       factor.
CC   -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed
CC       predominantly in the nucleoplasm. Interaction with ARF(P14)
CC       results in the localization of both proteins to the nucleolus. The
CC       nucleolar localization signals in both ARF(P14) and MDM2 may be
CC       necessary to allow efficient nucleolar localization of both
CC       proteins.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Mdm2-p90;
CC         IsoId=P23804-1; Sequence=Displayed;
CC         Note=Isoform Mdm2-p76 can also be produced by alternative
CC         initiation at Met-50 of isoform Mdm2-p90, but is produced more
CC         efficiently by alternative splicing;
CC       Name=Mdm2-p76;
CC         IsoId=P23804-2; Sequence=VSP_003215;
CC         Note=Does not bind to p53;
CC       Event=Alternative initiation;
CC         Comment=2 isoforms, Mdm2-p90 (shown here) and Mdm2-p76, are
CC         produced by alternative initiation at Met-1 and Met-50. Isoform
CC         Mdm2-p76 is produced more efficiently by alternative splicing;
CC   -!- TISSUE SPECIFICITY: Ubiquitously expressed at low-level throughout
CC       embryo development and in adult tissues. MDM2-p90 is much more
CC       abundant than MDM2-p76 in testis, brain, heart, and kidney, but in
CC       the thymus, spleen, and intestine, the levels of the MDM2 proteins
CC       are roughly equivalent.
CC   -!- INDUCTION: By UV light.
CC   -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its
CC       G1 arrest and apoptosis functions. It also binds p73 and E2F1.
CC       Region II contains most of a central acidic region required for
CC       interaction with ribosomal protein L5 and a putative C4-type zinc
CC       finger. The RING finger domain which coordinates two molecules of
CC       zinc interacts specifically with RNA whether or not zinc is
CC       present and mediates the hetero-oligomerization with MDM4. It is
CC       also essential for its ubiquitin ligase E3 activity toward p53 and
CC       itself.
CC   -!- PTM: Phosphorylated in response to ionizing radiation in an ATM-
CC       dependent manner.
CC   -!- DISEASE: The gene for this protein is amplified in a mouse tumor
CC       cell line.
CC   -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.
CC   -!- SIMILARITY: Contains 1 RanBP2-type zinc finger.
CC   -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC   -!- SIMILARITY: Contains 1 SWIB domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X58876; CAA41684.1; -.
DR   EMBL; U40145; AAA91167.1; -.
DR   EMBL; U47944; AAB09030.1; -.
DR   EMBL; U47935; AAB09030.1; JOINED.
DR   EMBL; U47936; AAB09030.1; JOINED.
DR   EMBL; U47937; AAB09030.1; JOINED.
DR   EMBL; U47938; AAB09030.1; JOINED.
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DR   EMBL; U47939; AAB09030.1; JOINED.
DR   EMBL; U47940; AAB09030.1; JOINED.
DR   EMBL; U47941; AAB09030.1; JOINED.
DR   EMBL; U47942; AAB09030.1; JOINED.
DR   EMBL; U47943; AAB09030.1; JOINED.
DR   EMBL; U47934; AAB09031.1; -.
DR   PIR; S15349; S15349.
DR   HSSP; Q9UMT8; 1YCR.
DR   MGD; MGI:96952; Mdm2.
DR   GO; GO:0005634; C:nucleus; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0004842; F:ubiquitin-protein ligase activity; IDA.
DR   GO; GO:0030163; P:protein catabolism; IDA.
DR   GO; GO:0016567; P:protein ubiquitination; IDA.
DR   GO; GO:0007089; P:traversing start control point of mitotic c. . .; IDA.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Alternative initiation; Alternative splicing; Ligase; Metal-binding;
KW   Nuclear protein; Phosphorylation; Proto-oncogene;
KW   Ubl conjugation pathway; Zinc; Zinc-finger.
FT   CHAIN         1    489       Ubiquitin-protein ligase E3 Mdm2, isoform
FT                                Mdm2-p90.
FT   CHAIN        50    489       ubiquitin-protein ligase E3 Mdm2, isoform
FT                                Mdm2-p76.
FT   INIT_MET      50     50       For isoform Mdm2-p76.
FT   DOMAIN        27    107       SWIB.
FT   DOMAIN       176    182       Nuclear localization signal (Potential).
FT   DOMAIN       183    195       Nuclear export signal.
FT   DOMAIN       203    213       Poly-Ser.
FT   DOMAIN       208    302       ARF-binding.
FT   DOMAIN       240    329       Region II.
FT   DOMAIN       221    299       Asp/Glu-rich (acidic).
FT   ZN_FING      297    326       RanBP2-type.
FT   ZN_FING      436    477       RING-type.
FT   DOMAIN       464    471       Nucleolar localization signal
FT                                (Potential).
FT   VARSPLIC       1     49       Missing (in isoform Mdm2-p76).
FT                                /FTId=VSP_003215.
FT   CONFLICT     203    203       S -> T (in Ref. 1).
FT   CONFLICT     419    419       D -> H (in Ref. 1).
FT   CONFLICT     486    486       S -> T (in Ref. 3).
SQ   SEQUENCE   489 AA;  54543 MW;  4ABF489E92038DF4 CRC64;

  Query Match             87.5%;  Score 485.5;  DB 1;  Length 489;
  Best Local Similarity   86.2%;  Pred. No. 3.6e-43;
  Matches   94;  Conservative    9;  Mismatches    3;  Indels    3;  Gaps    1;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||| ||||||:::|:||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQNDTYTMKEIIFYIGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||:|||||||||||||||| ||||||| |:||   |||||:||:
Db         77 CSNDLLGDVFGVPSFSVKEHRKIYAMIYRNLVAVSQQ---DSGTSLSES 122


RESULT 13
Q91XK7
ID   Q91XK7      PRELIMINARY;      PRT;   489 AA.
AC   Q91XK7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Mus musculus adult male lung cDNA, RIKEN full-length enriched library,
DE   clone:1200011P22 product:transformed mouse 3T3 cell double minute 2,
DE   full insert sequence (Transformed mouse 3T3 cell double minute 2) (Mus
DE   musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length
DE   enriched library, clone:E430022B10 product:transformed mouse 3T3 cell
DE   double minute 2, full insert sequence).
GN   Name=Mdm2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;
RX   MEDLINE=99279253; PubMed=10349636;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;
RX   MEDLINE=21085660; PubMed=11217851;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;
RX   MEDLINE=20499374; PubMed=11042159;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;
RX   MEDLINE=20530913; PubMed=11076861;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Lung;
RA   Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA   Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA   Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA   Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA   Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA   Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA   Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA   Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA   Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA   Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Mouse;
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RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [8]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Mouse;
RA   Strausberg R.;
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
RN   [9]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NOD; TISSUE=Thymus;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK004719; BAB23502.1; -.
DR   EMBL; BC050902; AAH50902.1; -.
DR   EMBL; AK088638; BAC40470.1; -.
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DR   MGD; MGI:96952; Mdm2.
DR   GO; GO:0005730; C:nucleolus; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0004842; F:ubiquitin-protein ligase activity; IDA.
DR   GO; GO:0030163; P:protein catabolism; IDA.
DR   GO; GO:0016567; P:protein ubiquitination; IDA.
DR   GO; GO:0007089; P:traversing start control point of mitotic c. . .; IDA.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB_MDM2.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
SQ   SEQUENCE   489 AA;  54557 MW;  4ABF489A82038DF4 CRC64;

  Query Match             87.5%;  Score 485.5;  DB 2;  Length 489;
  Best Local Similarity   86.2%;  Pred. No. 3.6e-43;
  Matches   94;  Conservative    9;  Mismatches    3;  Indels    3;  Gaps    1;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              |||||||||||||||||||||||||| |||||||:::|:||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQNDTYTMKEIIFYIGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
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Db         77 CSNDLLGDVFGVPSFSVKEHRKIYAMIYRNLVAVSQQ---DSGTSLSES 122


RESULT 14
Q8WYJ3
ID   Q8WYJ3      PRELIMINARY;      PRT;   118 AA.
AC   Q8WYJ3;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   MDM2 protein (Fragment).
GN   Name=MDM2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21248713; PubMed=11351297;
RA   Tamborini E., Della Torre G., Lavarino C., Azzarelli A.,
RA   Carpinelli P., Pierotti M.A., Pilotti S.;
RT   "Analysis of the molecular species generated by MDM2 gene
RT   amplification in liposarcomas.";
RL   Int. J. Cancer 92:790-796(2001).
DR   EMBL; AF092843; AAL40178.1; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB_MDM2.
DR   Pfam; PF02201; SWIB; 1.
FT   NON_TER     118    118
SQ   SEQUENCE   118 AA;  13536 MW;  D7A4DBAA83D8841B CRC64;

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Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVV 93
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Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVV 109


RESULT 15
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ID   MDM2_MESAU     STANDARD;      PRT;   466 AA.
AC   Q60524;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein
DE   Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Fragment).
GN   Name=MDM2;
OS   Mesocricetus auratus (Golden hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC   Mesocricetus.
OX   NCBI_TaxID=10036;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pancreas;
RX   MEDLINE=95300112; PubMed=7780969;
RA   Chang K.W., Laconi S., Mangold K.A., Hubchak S., Scarpelli D.G.;
RT   "Multiple genetic alterations in hamster pancreatic ductal
RT   adenocarcinomas.";
RL   Cancer Res. 55:2560-2568(1995).
CC   -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC       apoptosis by binding its transcriptional activation domain.
CC       Functions as a ubiquitin ligase E3, in the presence of E1 and E2,
CC       toward p53 and itself. Permits the nuclear export of p53 and
```

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CC       targets it for proteasome-mediated proteolysis (By similarity).
CC   -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity (By
CC       similarity).
CC   -!- SUBUNIT: Binds p53, p73, ARF(P14), ribosomal protein L5 and
CC       specifically to RNA. Can interact also with retinoblastoma protein
CC       (RB), E1A-associated protein EP300 and the E2F1 transcription
CC       factor (By similarity).
CC   -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed
CC       predominantly in the nucleoplasm (By similarity).
CC   -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its
CC       G1 arrest and apoptosis functions. It also binds p73 and E2F1.
CC       Region II contains most of a central acidic region required for
CC       interaction with ribosomal protein L5 and a putative C4-type zinc
CC       finger. The RING finger domain which coordinates two molecules of
CC       zinc interacts specifically with RNA whether or not zinc is
CC       present and mediates the hetero-oligomerization with MDM4. It is
CC       also essential for its ubiquitin ligase E3 activity toward p53 and
CC       itself (By similarity).
CC   -!- DISEASE: The gene for this protein is overexpressed in some
CC       tumors.
CC   -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.
CC   -!- SIMILARITY: Contains 1 RanBP2-type zinc finger.
CC   -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC   -!- SIMILARITY: Contains 1 SWIB domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
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DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Ligase; Metal-binding; Nuclear protein; Proto-oncogene;
KW   Ubl conjugation pathway; Zinc; Zinc-finger.
FT   NON_TER       1      1
FT   DOMAIN       19     98       SWIB.
FT   DOMAIN      169    175       Nuclear localization signal (Potential).
FT   DOMAIN      176    188       Nuclear export signal.
FT   DOMAIN      196    201       Poly-Ser.
FT   DOMAIN      196    290       ARF-binding.
FT   DOMAIN      228    317       Region II.
FT   DOMAIN      209    287       Asp/Glu-rich (acidic).
FT   ZN_FING     285    314       RanBP2-type.
FT   ZN_FING     419    460       RING-type.
FT   DOMAIN      447    454       Nucleolar localization signal
FT                                (Potential).
FT   NON_TER     466    466
SQ   SEQUENCE   466 AA;  52390 MW;  78A3042163C5F939 CRC64;

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Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
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GenCore version 5.1.6

OM protein - protein search, using sw model

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Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	545	98.2	188	4	US-09-603-052-4	Sequence 4, Appli
2	545	98.2	491	1	US-07-903-103-2	Sequence 2, Appli
3	545	98.2	491	1	US-08-044-619A-2	Sequence 2, Appli
4	545	98.2	491	1	US-08-283-911-2	Sequence 2, Appli
5	545	98.2	491	1	US-08-245-500A-3	Sequence 3, Appli
6	545	98.2	491	1	US-08-390-546-3	Sequence 3, Appli
7	545	98.2	491	1	US-08-390-479A-3	Sequence 3, Appli
8	545	98.2	491	1	US-08-557-393-3	Sequence 3, Appli
9	545	98.2	491	1	US-08-390-516C-3	Sequence 3, Appli
10	545	98.2	491	1	US-08-390-517A-3	Sequence 3, Appli
11	545	98.2	491	1	US-08-390-515A-3	Sequence 3, Appli
12	545	98.2	491	2	US-08-801-718-3	Sequence 3, Appli
13	545	98.2	491	3	US-09-170-159A-3	Sequence 3, Appli
14	545	98.2	491	4	US-09-480-718-44	Sequence 44, Appl
15	528.5	95.2	216	3	US-09-510-252-4	Sequence 4, Appli
16	485.5	87.5	489	1	US-07-903-103-4	Sequence 4, Appli
17	485.5	87.5	489	1	US-08-044-619A-4	Sequence 4, Appli
18	485.5	87.5	489	1	US-08-283-911-4	Sequence 4, Appli
19	485.5	87.5	489	1	US-08-245-500A-5	Sequence 5, Appli
20	485.5	87.5	489	1	US-08-390-546-5	Sequence 5, Appli
21	485.5	87.5	489	1	US-08-390-479A-5	Sequence 5, Appli
22	485.5	87.5	489	1	US-08-557-393-5	Sequence 5, Appli
23	485.5	87.5	489	1	US-08-390-516C-5	Sequence 5, Appli
24	485.5	87.5	489	1	US-08-390-517A-5	Sequence 5, Appli
25	485.5	87.5	489	1	US-08-390-515A-5	Sequence 5, Appli
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27	485.5	87.5	489	3	US-09-170-159A-5	Sequence 5, Appli
28	485.5	87.5	489	4	US-09-480-718-46	Sequence 46, Appl
29	176	31.7	243	4	US-09-786-702-2	Sequence 2, Appli
30	73.5	13.2	244	4	US-09-543-681A-6675	Sequence 6675, Ap
31	71.5	12.9	420	4	US-09-270-767-43304	Sequence 43304, A
32	66.5	12.0	104	4	US-09-270-767-41801	Sequence 41801, A
33	66.5	12.0	590	3	US-09-232-191-25	Sequence 25, Appl
34	66.5	12.0	590	3	US-09-232-200-75	Sequence 75, Appl
35	66.5	12.0	590	3	US-09-232-197-75	Sequence 75, Appl
36	66.5	12.0	590	3	US-09-232-201-75	Sequence 75, Appl
37	66.5	12.0	590	4	US-09-232-195-75	Sequence 75, Appl
38	65	11.7	384	4	US-08-504-617-2	Sequence 2, Appli
39	65	11.7	766	4	US-09-248-796A-16626	Sequence 16626, A
40	64.5	11.6	253	4	US-09-270-767-38412	Sequence 38412, A
41	64.5	11.6	253	4	US-09-270-767-53629	Sequence 53629, A
42	64.5	11.6	482	4	US-09-248-796A-17755	Sequence 17755, A
43	64.5	11.6	1432	3	US-08-781-891-71	Sequence 71, Appl
44	64.5	11.6	1432	4	US-09-618-166-71	Sequence 71, Appl
45	64.5	11.6	2184	4	US-09-417-485D-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-603-052-4
; Sequence 4, Application US/09603052
; Patent No. 6492116
; GENERAL INFORMATION:
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; TITLE OF INVENTION: Assay for identifying inhibitors of the interaction
; TITLE OF INVENTION: between proteins p53 and dm2
; FILE REFERENCE: MEWB26.001C1
; CURRENT APPLICATION NUMBER: US/09/603,052
; CURRENT FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: EP 95810576.9
; PRIOR FILING DATE: 1995-09-18
; PRIOR APPLICATION NUMBER: PCT/EP96/03957
; PRIOR FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-603-052-4

Query Match 98.2%; Score 545; DB 4; Length 188;
Best Local Similarity 98.2%; Pred. No. 8.4e-60;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
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RESULT 2
US-07-903-103-2
; Sequence 2, Application US/07903103
; Patent No. 5411860
; GENERAL INFORMATION:
; APPLICANT: VOGELSTEIN, BERT
; APPLICANT: KINZLER, KENNETH
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G ST., N.W.

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;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001-4597
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/903,103
;      FILING DATE:  19920623
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/867.840
;      FILING DATE:  07-APR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.40148
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-903-103-2

  Query Match             98.2%;  Score 545;  DB 1;  Length 491;
  Best Local Similarity   98.2%;  Pred. No. 3e-59;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 3
US-08-044-619A-2
; Sequence 2, Application US/08044619A
; Patent No. 5420263
;  GENERAL INFORMATION:
;    APPLICANT:  THE JOHNS HOPKINS UNIVERSITY
;    APPLICANT:  720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G ST., N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001-4597
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/044,619A
;      FILING DATE:  07-APR-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/903,103
;      FILING DATE:  23-JUN-1992
;      APPLICATION NUMBER:  US 07/867.840
;      FILING DATE:  07-APR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.40148
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-044-619A-2

  Query Match             98.2%;  Score 545;  DB 1;  Length 491;
  Best Local Similarity   98.2%;  Pred. No. 3e-59;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 4
US-08-283-911-2
; Sequence 2, Application US/08283911
; Patent No. 5519118
;  GENERAL INFORMATION:
;    APPLICANT:  VOGELSTEIN, BERT
;    APPLICANT:  KINZLER, KENNETH
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G ST., N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001-4597
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/283,911
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/903,103
;      FILING DATE:  23-JUN-1992
;      APPLICATION NUMBER:  US 07/867.840
;      FILING DATE:  07-APR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.40148
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-283-911-2

  Query Match             98.2%;  Score 545;  DB 1;  Length 491;
  Best Local Similarity   98.2%;  Pred. No. 3e-59;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 5
US-08-245-500A-3
; Sequence 3, Application US/08245500A
; Patent No. 5550023
;  GENERAL INFORMATION:
;    APPLICANT:  BURRELL, MARILEE
;    APPLICANT:  HILL, DAVID E.
;    APPLICANT:  KINZLER, KENNETH W.
;    APPLICANT:  VOGELSTEIN, BERT
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/245,500A
;      FILING DATE:  07-APR-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.42798
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-245-500A-3

  Query Match             98.2%;  Score 545;  DB 1;  Length 491;
  Best Local Similarity   98.2%;  Pred. No. 3e-59;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 6
US-08-390-546-3
; Sequence 3, Application US/08390546
; Patent No. 5606044
;  GENERAL INFORMATION:
;    APPLICANT:  BURRELL, MARILEE
;    APPLICANT:  HILL, DAVID E.
;    APPLICANT:  KINZLER, KENNETH W.
;    APPLICANT:  VOGELSTEIN, BERT
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/390,546
;      FILING DATE:  07-APR-1993
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.42798
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-390-546-3

  Query Match             98.2%;  Score 545;  DB 1;  Length 491;
  Best Local Similarity   98.2%;  Pred. No. 3e-59;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 7
US-08-390-479A-3
; Sequence 3, Application US/08390479A
; Patent No. 5618921
;  GENERAL INFORMATION:
;    APPLICANT:  BURRELL, MARILEE
;    APPLICANT:  HILL, DAVID E.
;    APPLICANT:  KINZLER, KENNETH W.
;    APPLICANT:  VOGELSTEIN, BERT
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
```

```
;      ADDRESSEE:  BANNER & WITCOFF, LTD.
;      STREET:  1001 G STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/390,479A
;      FILING DATE:  02-FEB-1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.48992
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-390-479A-3

  Query Match             98.2%;  Score 545;  DB 1;  Length 491;
  Best Local Similarity   98.2%;  Pred. No. 3e-59;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 8
US-08-557-393-3
; Sequence 3, Application US/08557393
; Patent No. 5702903
;  GENERAL INFORMATION:
;    APPLICANT:  BURRELL, MARILEE
;    APPLICANT:  HILL, DAVID E.
;    APPLICANT:  KINZLER, KENNETH W.
;    APPLICANT:  VOGELSTEIN, BERT
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/557,393
;      FILING DATE:  13-NOV-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/245,500
;      FILING DATE:  18-MAY-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.42798
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-557-393-3

  Query Match             98.2%;  Score 545;  DB 1;  Length 491;
  Best Local Similarity   98.2%;  Pred. No. 3e-59;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 9
US-08-390-516C-3
; Sequence 3, Application US/08390516C
; Patent No. 5708136
;  GENERAL INFORMATION:
;    APPLICANT:  BURRELL, MARILEE
;    APPLICANT:  HILL, DAVID E.
;    APPLICANT:  KINZLER, KENNETH W.
;    APPLICANT:  VOGELSTEIN, BERT
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/390,516C
;      FILING DATE:  07-APR-1993
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.42798
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
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US-08-390-516C-3

Query Match 98.2%; Score 545; DB 1; Length 491;
Best Local Similarity 98.2%; Pred. No. 3e-59;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125
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RESULT 10
US-08-390-517A-3
; Sequence 3, Application US/08390517A
; Patent No. 5736338
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,517A
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-390-517A-3

Query Match 98.2%; Score 545; DB 1; Length 491;
Best Local Similarity 98.2%; Pred. No. 3e-59;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125
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RESULT 11

US-08-390-515A-3
; Sequence 3, Application US/08390515A
; Patent No. 5756455
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,515A
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-390-515A-3

Query Match 98.2%; Score 545; DB 1; Length 491;
Best Local Similarity 98.2%; Pred. No. 3e-59;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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RESULT 12
US-08-801-718-3
; Sequence 3, Application US/08801718
; Patent No. 5858976
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.

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;       COUNTRY:  USA
;       ZIP:  20001
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/801,718
;       FILING DATE:  14-FEB-1997
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/390,515
;       FILING DATE:  07-APR-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  KAGAN, SARAH A.
;       REGISTRATION NUMBER:  32,141
;       REFERENCE/DOCKET NUMBER:  01107.42798
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-508-9100
;       TELEFAX:  202-508-9299
;       TELEX:  197430 BBMB UT
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  491 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-801-718-3

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RESULT 13
US-09-170-159A-3
; Sequence 3, Application US/09170159A
; Patent No. 6399755
;   GENERAL INFORMATION:
;       APPLICANT: BURRELL, MARILEE
;                  HILL, DAVID E.
;                  KINZLER, KENNETH W.
;                  VOGELSTEIN, BERT
;       TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
;                           HUMAN TUMORS
;       NUMBER OF SEQUENCES: 5
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
;            STREET: 1001 G STREET, N.W.
;            CITY: WASHINGTON
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20001
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/170,159A
;            FILING DATE: 13-Oct-1998
;            CLASSIFICATION: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: KAGAN, SARAH A.
;            REGISTRATION NUMBER: 32,141
;            REFERENCE/DOCKET NUMBER: 01107.42798
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-508-9100
;            TELEFAX: 202-508-9299
;            TELEX: 197430 BBMB UT
;   INFORMATION FOR SEQ ID NO: 3:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 491 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-170-159A-3

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RESULT 14
US-09-480-718-44
; Sequence 44, Application US/09480718
; Patent No. 6407062
; GENERAL INFORMATION:
;  APPLICANT: Sherr, Charles J
;  APPLICANT: Quelle, Dawn E
;  APPLICANT: Weber, Jason D.
;  APPLICANT: Roussel, Martine F.
;  APPLICANT: Frederique, Zindy
;  TITLE OF INVENTION: ARF-19, A NOVEL REGULATOR OF THE MAMMALIAN CELL CYCLE
;  FILE REFERENCE: 1340-1-023 CIP 1
;  CURRENT APPLICATION NUMBER: US/09/480,718
;  CURRENT FILING DATE: 2000-01-07
;  EARLIER APPLICATION NUMBER: 09/129,855
;  EARLIER FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-480-718-44

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RESULT 15
US-09-510-252-4
; Sequence 4, Application US/09510252
; Patent No. 6372490
; GENERAL INFORMATION:
;  APPLICANT: Nandabalan, Krishnan
;  APPLICANT:  Yang, Meijia
;  APPLICANT:  Schulz, Vincent
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;  APPLICANT:  CuraGen Corporation
;  TITLE OF INVENTION: MDM INTERACTING PROTEIN AND METHODS OF USE THEREOF
;  FILE REFERENCE: 15966-524 MDM US
;  CURRENT APPLICATION NUMBER: US/09/510,252
;  CURRENT FILING DATE:  2000-02-22
;  PRIOR APPLICATION NUMBER: USSN 60/121,192
;  PRIOR FILING DATE: 1999-02-23
;  PRIOR APPLICATION NUMBER: USSN 60/122,643
;  PRIOR FILING DATE: 1999-03-03
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 216
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-510-252-4

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OM protein - protein search, using sw model

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Perfect score: 555
Sequence: 1 SQIPASEQETLVRPKPLLLK.....NLVVVNQQESSDSGTSVSEN 109

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	545	98.2	491	9	US-09-956-425-8	Sequence 8, Appli
3	545	98.2	491	10	US-09-029-327-2	Sequence 2, Appli
4	545	98.2	491	11	US-09-966-724-2	Sequence 2, Appli
5	545	98.2	491	15	US-10-422-536-137	Sequence 137, App
6	545	98.2	491	15	US-10-232-951-35	Sequence 35, Appl
7	545	98.2	491	17	US-10-685-838-1	Sequence 1, Appli
8	545	98.2	491	17	US-10-724-225-2	Sequence 2, Appli
9	545	98.2	491	17	US-10-489-802-8	Sequence 8, Appli
10	545	98.2	491	17	US-10-723-860-2236	Sequence 2236, Ap
11	528.5	95.2	216	13	US-10-057-510-4	Sequence 4, Appli
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13	519.5	93.6	522	15	US-10-287-226-382	Sequence 382, App
14	485.5	87.5	489	9	US-09-956-425-6	Sequence 6, Appli
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19	465	83.8	92	17	US-10-685-838-3	Sequence 3, Appli
20	306	55.1	59	14	US-10-211-088-143	Sequence 143, App
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23	72	13.0	967	15	US-10-282-122A-59020	Sequence 59020, A
24	71	12.8	472	14	US-10-369-493-16585	Sequence 16585, A
25	71	12.8	473	15	US-10-282-122A-45311	Sequence 45311, A
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27	70.5	12.7	467	14	US-10-369-493-6071	Sequence 6071, Ap
28	70	12.6	969	15	US-10-335-977-7409	Sequence 7409, Ap
29	70	12.6	972	15	US-10-335-977-7410	Sequence 7410, Ap
30	69.5	12.5	328	17	US-10-425-115-191466	Sequence 191466,
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32	69.5	12.5	709	15	US-10-282-122A-63455	Sequence 63455, A
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34	68	12.3	438	14	US-10-176-584A-2	Sequence 2, Appli
35	68	12.3	705	15	US-10-425-114-57081	Sequence 57081, A
36	68	12.3	705	17	US-10-425-115-365082	Sequence 365082,
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40	67.5	12.2	350	10	US-09-746-783-54	Sequence 54, Appl
41	67.5	12.2	422	14	US-10-369-493-7027	Sequence 7027, Ap
42	67.5	12.2	837	16	US-10-408-765A-2452	Sequence 2452, Ap
43	67	12.1	368	15	US-10-389-566-382	Sequence 382, App
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ALIGNMENTS

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; Sequence 1, Application US/09888077
; Patent No. US20020031818A1
; GENERAL INFORMATION:
; APPLICANT: Ronai, Ze'ev
; APPLICANT: Fuchs, Serge
; TITLE OF INVENTION: Modification of Mdm2 Activity
; FILE REFERENCE: 2420/1H195-US1
; CURRENT APPLICATION NUMBER: US/09/888,077
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,343
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-888-077-1

Query Match 98.2%; Score 545; DB 9; Length 491;
Best Local Similarity 98.2%; Pred. No. 2.9e-55;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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; Sequence 8, Application US/09956425
; Patent No. US20020045192A1
; GENERAL INFORMATION:
;  APPLICANT: Kriwacki, Richard
;  APPLICANT:  Bothner, Brian
;  APPLICANT:  Lewis, William
;  TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and Method of Use Thereof
;  FILE REFERENCE: 1340/1/035
;  CURRENT APPLICATION NUMBER: US/09/956,425
;  CURRENT FILING DATE:  2001-09-19
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-956-425-8

  Query Match             98.2%;  Score 545;  DB 9;  Length 491;
  Best Local Similarity   98.2%;  Pred. No. 2.9e-55;
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RESULT 3
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; Sequence 2, Application US/09029327
; Publication No. US20030060432A1
;  GENERAL INFORMATION:
;    APPLICANT:  TOCQUE, Bruno
;    APPLICANT:  WASYLYK, Bohdan
;    APPLICANT:  DUBS-POTERSZMAN,
;    APPLICANT:  Marie-Christine
;    TITLE OF INVENTION:  ANTAGONISTS OF THE ONCOGENIC ACTIVITY OF
;    TITLE OF INVENTION:  THE PROTEIN MDM2, AND USE THEREOF IN THE TREATMENT OF
;    TITLE OF INVENTION:  CANCERS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rhone-Poulenc Rorer Inc.
;      STREET:  500 Arcola Road, Mailstop 3C43
;      CITY:  Collegeville
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19426
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/029,327
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR 96/01340
;      FILING DATE:  02-SEP-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO FR95/10331
;      FILING DATE:  04-SEP-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fehlner Esq., Paul F.
;      REGISTRATION NUMBER:  35,135
;      REFERENCE/DOCKET NUMBER:  ST95050-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (610) 454-3839
;      TELEFAX:  (610) 454-3808
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-029-327-2

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  Best Local Similarity   98.2%;  Pred. No. 2.9e-55;
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; Sequence 2, Application US/09966724
; Publication No. US20040170971A1
;  GENERAL INFORMATION:
;       APPLICANT: THE JOHNS HOPKINS UNIVERSITY
;                  720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA
;       TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
;                           HUMAN TUMORS
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
;            STREET: 1001 G ST., N.W.
;            CITY: WASHINGTON
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20001-4597
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/966,724
;            FILING DATE: 01-Oct-2001
;            CLASSIFICATION: 435
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/044,619
;            FILING DATE: 2001-10-01
;            APPLICATION NUMBER: US 07/867.840
;            FILING DATE: 07-APR-1992
;       ATTORNEY/AGENT INFORMATION:
;            NAME: KAGAN, SARAH A.
;            REGISTRATION NUMBER: 32,141
;            REFERENCE/DOCKET NUMBER: 01107.40148
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-508-9100
;            TELEFAX: 202-508-9299
;            TELEX: 197430 BBMB UT
;  INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 491 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-966-724-2

  Query Match             98.2%;  Score 545;  DB 11;  Length 491;
  Best Local Similarity   98.2%;  Pred. No. 2.9e-55;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 5
US-10-422-536-137
; Sequence 137, Application US/10422536
; Publication No. US20040014100A1
; GENERAL INFORMATION:
;  APPLICANT: Kinsella, Todd
;  APPLICANT:  Lorens, James
;  APPLICANT:  Pray, Todd
;  APPLICANT:  Bennett, Mark
;  TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR INHIBITING
;  TITLE OF INVENTION:  PROTEIN-PROTEIN INTERACTION
;  FILE REFERENCE: A-71433-1/AMP/CYO
;  CURRENT APPLICATION NUMBER: US/10/422,536
;  CURRENT FILING DATE:  2003-04-23
;  PRIOR APPLICATION NUMBER: US 60/187,130
;  PRIOR FILING DATE: 2000-03-06
;  PRIOR APPLICATION NUMBER: US 09/800,770
;  PRIOR FILING DATE: 2001-03-06
;  PRIOR APPLICATION NUMBER: US 10/232,758
;  PRIOR FILING DATE: 2002-08-30
;  NUMBER OF SEQ ID NOS: 168
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 137
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-422-536-137

  Query Match             98.2%;  Score 545;  DB 15;  Length 491;
  Best Local Similarity   98.2%;  Pred. No. 2.9e-55;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 6
US-10-232-951-35
; Sequence 35, Application US/10232951
; Publication No. US20040043386A1
; GENERAL INFORMATION:
;  APPLICANT: Pray, Todd
;  APPLICANT:  Wong, Brian
;  APPLICANT:  Bennett, Mark
;  APPLICANT:  Parlati, Francesco
;  APPLICANT:  Rigel Pharmaceuticals, Incorporated
;  TITLE OF INVENTION: Methods and Compositions for Functional Ubiquitin
;  TITLE OF INVENTION:  Assays
;  FILE REFERENCE: 021044-006800US
;  CURRENT APPLICATION NUMBER: US/10/232,951
;  CURRENT FILING DATE:  2002-08-30
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: E3 ubiquitin ligating agent mouse double minute 2
;   OTHER INFORMATION: (mdm2) homolog full length protein isoform, mouse
;   OTHER INFORMATION: p53-binding protein (MDM2) homolog, transcript
;   OTHER INFORMATION: variant MDM2, transformed 3T3 cell double minute 2,
;   OTHER INFORMATION: Mdm2 cDNA
US-10-232-951-35

  Query Match             98.2%;  Score 545;  DB 15;  Length 491;
  Best Local Similarity   98.2%;  Pred. No. 2.9e-55;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 7
US-10-685-838-1
; Sequence 1, Application US/10685838
; Publication No. US20040197893A1
; GENERAL INFORMATION:
;  APPLICANT: SHUBERT, CARSTEN
;  APPLICANT:  GRASBERGER, BRUCE
;  APPLICANT:  MAGUIRE, DIANE
;  APPLICANT:  DECKMAN, INGRID
;  APPLICANT:  SPURLINO, JOHN
;  TITLE OF INVENTION: HDM2-INHIBITOR COMPLEXES AND USES THEREOF
;  FILE REFERENCE: PRD-2137-USANP
;  CURRENT APPLICATION NUMBER: US/10/685,838
;  CURRENT FILING DATE:  2003-10-15
;  PRIOR APPLICATION NUMBER: 60/418,350
;  PRIOR FILING DATE: 2002-10-16
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-685-838-1

  Query Match             98.2%;  Score 545;  DB 17;  Length 491;
  Best Local Similarity   98.2%;  Pred. No. 2.9e-55;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 8
US-10-724-225-2
; Sequence 2, Application US/10724225
; Publication No. US20040209834A1
;   GENERAL INFORMATION:
;        APPLICANT: TOCQUE, Bruno
;                   WASYLYK, Bohdan
;                   DUBS-POTERSZMAN,
;                   Marie-Christine
;        TITLE OF INVENTION: ANTAGONISTS OF THE ONCOGENIC ACTIVITY OF
;                            THE PROTEIN MDM2, AND USE THEREOF IN THE TREATMENT OF
;                            CANCERS
;        NUMBER OF SEQUENCES: 4
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Rhone-Poulenc Rorer Inc.
;             STREET: 500 Arcola Road, Mailstop 3C43
;             CITY: Collegeville
```

```
;              STATE: PA
;              COUNTRY: USA
;              ZIP: 19426
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/10/724,225
;              FILING DATE: 01-Dec-2003
;              CLASSIFICATION: 514
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: US/09/029,327
;              FILING DATE: <Unknown>
;              APPLICATION NUMBER: FR 96/01340
;              FILING DATE: 02-SEP-1996
;              APPLICATION NUMBER: WO FR95/10331
;              FILING DATE: 04-SEP-1995
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Fehlner Esq., Paul F.
;              REGISTRATION NUMBER: 35,135
;              REFERENCE/DOCKET NUMBER: ST95050-US
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (610) 454-3839
;              TELEFAX: (610) 454-3808
;    INFORMATION FOR SEQ ID NO: 2:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 491 amino acids
;              TYPE: amino acid
;              TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-724-225-2

  Query Match             98.2%;  Score 545;  DB 17;  Length 491;
  Best Local Similarity   98.2%;  Pred. No. 2.9e-55;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              |||||||||||||||||||||||||||||||||||||:||||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 9
US-10-489-802-8
; Sequence 8, Application US/10489802
; Publication No. US20040248198A1
; GENERAL INFORMATION:
;  APPLICANT: St. Jude Children's Research Hospital, Inc.
;  APPLICANT:  Kriwacki, Richard
;  APPLICANT:  Bothner, Brian
;  APPLICANT:  Lewis, William
;  TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and
;  TITLE OF INVENTION:  Method of Use Thereof
;  FILE REFERENCE: 44158/243642
;  CURRENT APPLICATION NUMBER: US/10/489,802
;  CURRENT FILING DATE:  2004-03-16
;  PRIOR APPLICATION NUMBER: US 09/956,425
;  PRIOR FILING DATE: 2001-09-19
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-489-802-8

  Query Match             98.2%;  Score 545;  DB 17;  Length 491;
  Best Local Similarity   98.2%;  Pred. No. 2.9e-55;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              |||||||||||||||||||||||||||||||||||||:||||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 10
US-10-723-860-2236
; Sequence 2236, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
;  APPLICANT: Aziz, Natasha
;  APPLICANT:  Ginsburg, Wendy M.
;  APPLICANT:  Zlotnik, Albert
;  TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
;  TITLE OF INVENTION:  Methods for Screening for Soft Tissue Sarcoma Modulators
;  FILE REFERENCE: 05882.0193.NPUS01
;  CURRENT APPLICATION NUMBER: US/10/723,860
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: 60/429,739
;  PRIOR FILING DATE: 2002-11-26
;  NUMBER OF SEQ ID NOS: 8393
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2236
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-723-860-2236

  Query Match             98.2%;  Score 545;  DB 17;  Length 491;
  Best Local Similarity   98.2%;  Pred. No. 2.9e-55;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              |||||||||||||||||||||||||||||||||||||:||||||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 11
US-10-057-510-4
; Sequence 4, Application US/10057510
; Publication No. US20020098580A1
; GENERAL INFORMATION:
;  APPLICANT: Nandabalan, Krishnan
;  APPLICANT:  Yang, Meijia
;  APPLICANT:  Schulz, Vincent
;  APPLICANT:  CuraGen Corporation
;  TITLE OF INVENTION: MDM INTERACTING PROTEIN AND METHODS OF USE THEREOF
;  FILE REFERENCE: 15966-524 MDM US
;  CURRENT APPLICATION NUMBER: US/10/057,510
;  CURRENT FILING DATE:  2002-01-25
;  PRIOR APPLICATION NUMBER: USSN 09/510,252
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: USSN 60/121,192
;  PRIOR FILING DATE: 1999-02-23
;  PRIOR APPLICATION NUMBER: USSN 60/122,643
;  PRIOR FILING DATE: 1999-03-03
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 216
;   TYPE: PRT
;   ORGANISM: Homo sapiens
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US-10-057-510-4

  Query Match             95.2%;  Score 528.5;  DB 13;  Length 216;
  Best Local Similarity   97.2%;  Pred. No. 8.6e-54;
  Matches  106;  Conservative    2;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              ||||||||||||||||||||||||||||||||||||||:|| ||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYL-QYIMTKRLYDEKQQHIVY 75

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 124


RESULT 12
US-10-287-226-380
; Sequence 380, Application US/10287226
; Publication No. US20040086875A1
; GENERAL INFORMATION:
;  APPLICANT: Agee, Michele L.,
;  APPLICANT:  Alsobrook, John P.,
;  APPLICANT:  Berghs, Constance,
;  APPLICANT:  Boldog, Ference,
;  APPLICANT:  Burgess, Catherine E.,
;  APPLICANT:  Chant, John S.,
;  APPLICANT:  Chaudhuri, Amitabha,
;  APPLICANT:  DiPippo, Vincent A.,
;  APPLICANT:  Edinger, Shlomit R.,
;  APPLICANT:  Eisen, Andrew,
;  APPLICANT:  Ellerman, Karen,
;  APPLICANT:  Gangolli, Esha A.,
;  APPLICANT:  Gorman, Linda,
;  APPLICANT:  Gerlach, Valerie,
;  APPLICANT:  Ji, Weizhen,
;  APPLICANT:  Kekuda, Ramesh,
;  APPLICANT:  Khramtsov, Nikolai,
;  APPLICANT:  Li, Li,
;  APPLICANT:  Malyankar, Uriel M.,
;  APPLICANT:  MacDougall, John R.,
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Miller, Charles E.,
;  APPLICANT:  Millet, Isabelle,
;  APPLICANT:  Ooi, Chean Eng,
;  APPLICANT:  Ort, Tatiana,
;  APPLICANT:  Padigaru, Muralidhara,
;  APPLICANT:  Patturajan, Meera,
;  APPLICANT:  Rastelli, Luca,
;  APPLICANT:  Rieger, Daniel K.,
;  APPLICANT:  Rothenberg, Mark E.,
;  APPLICANT:  Shenoy, Suresh G.,
;  APPLICANT:  Spaderna, Steven K.,
;  APPLICANT:  Spytek, Kimberley A.,
;  APPLICANT:  Taupier, Jr., Raymond J.,
;  APPLICANT:  Vernet, Corine A.M.,
;  APPLICANT:  Zerhusen, Bryan D.,
;  APPLICANT:  Zhong, Mei
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-480C
;  CURRENT APPLICATION NUMBER: US/10/287,226
;  CURRENT FILING DATE:  2002-11-04
;  PRIOR APPLICATION NUMBER: 60/334,421
;  PRIOR FILING DATE: 2001-11-30
;  PRIOR APPLICATION NUMBER: 60/354,392
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: 60/360,148
;  PRIOR FILING DATE: 2002-02-27
;  PRIOR APPLICATION NUMBER: 60/364,000
;  PRIOR FILING DATE: 2002-03-13
;  PRIOR APPLICATION NUMBER: 60/404,821
;  PRIOR FILING DATE: 2002-08-20
;  PRIOR APPLICATION NUMBER: 60/334,526
;  PRIOR FILING DATE: 2001-11-30
;  PRIOR APPLICATION NUMBER: 60/354,409
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: 60/364,227
;  PRIOR FILING DATE: 2002-03-13
;  PRIOR APPLICATION NUMBER: 60/334,027
;  PRIOR FILING DATE: 2001-11-28
;  PRIOR APPLICATION NUMBER: 60/331,641
;  PRIOR FILING DATE: 2001-11-20
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 673
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 380
;   LENGTH: 522
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-287-226-380

  Query Match             93.6%;  Score 519.5;  DB 15;  Length 522;
  Best Local Similarity   76.4%;  Pred. No. 3.1e-52;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels   31;  Gaps    1;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKE---------------------- 36
              ||||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKERWSFTMLPRLVWNSWAQGICLPRP 76

Qy         37 -------VLYYLGQYIMTKRLYDEKQQHIVHCSNDLLGDLFGVPSFSVKEHRKIYTMIYR 89
                    ||:|||||||||||||||||:|||||||||||||||||||||||||||||
Db         77 PKVLDLQVLFYLGQYIMTKRLYDEKQQHIVYCSNDLLGDLFGVPSFSVKEHRKIYTMIYR 136

Qy         90 NLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||
Db        137 NLVVVNQQESSDSGTSVSEN 156


RESULT 13
US-10-287-226-382
; Sequence 382, Application US/10287226
; Publication No. US20040086875A1
; GENERAL INFORMATION:
;  APPLICANT: Agee, Michele L.,
;  APPLICANT:  Alsobrook, John P.,
;  APPLICANT:  Berghs, Constance,
;  APPLICANT:  Boldog, Ference,
;  APPLICANT:  Burgess, Catherine E.,
;  APPLICANT:  Chant, John S.,
;  APPLICANT:  Chaudhuri, Amitabha,
;  APPLICANT:  DiPippo, Vincent A.,
;  APPLICANT:  Edinger, Shlomit R.,
;  APPLICANT:  Eisen, Andrew,
;  APPLICANT:  Ellerman, Karen,
;  APPLICANT:  Gangolli, Esha A.,
;  APPLICANT:  Gorman, Linda,
;  APPLICANT:  Gerlach, Valerie,
;  APPLICANT:  Ji, Weizhen,
;  APPLICANT:  Kekuda, Ramesh,
;  APPLICANT:  Khramtsov, Nikolai,
;  APPLICANT:  Li, Li,
;  APPLICANT:  Malyankar, Uriel M.,
;  APPLICANT:  MacDougall, John R.,
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Miller, Charles E.,
;  APPLICANT:  Millet, Isabelle,
;  APPLICANT:  Ooi, Chean Eng,
;  APPLICANT:  Ort, Tatiana,
;  APPLICANT:  Padigaru, Muralidhara,
;  APPLICANT:  Patturajan, Meera,
;  APPLICANT:  Rastelli, Luca,
;  APPLICANT:  Rieger, Daniel K.,
;  APPLICANT:  Rothenberg, Mark E.,
;  APPLICANT:  Shenoy, Suresh G.,
;  APPLICANT:  Spaderna, Steven K.,
;  APPLICANT:  Spytek, Kimberley A.,
;  APPLICANT:  Taupier, Jr., Raymond J.,
```

```
;  APPLICANT:  Vernet, Corine A.M.,
;  APPLICANT:  Zerhusen, Bryan D.,
;  APPLICANT:  Zhong, Mei
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-480C
;  CURRENT APPLICATION NUMBER: US/10/287,226
;  CURRENT FILING DATE:  2002-11-04
;  PRIOR APPLICATION NUMBER: 60/334,421
;  PRIOR FILING DATE: 2001-11-30
;  PRIOR APPLICATION NUMBER: 60/354,392
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: 60/360,148
;  PRIOR FILING DATE: 2002-02-27
;  PRIOR APPLICATION NUMBER: 60/364,000
;  PRIOR FILING DATE: 2002-03-13
;  PRIOR APPLICATION NUMBER: 60/404,821
;  PRIOR FILING DATE: 2002-08-20
;  PRIOR APPLICATION NUMBER: 60/334,526
;  PRIOR FILING DATE: 2001-11-30
;  PRIOR APPLICATION NUMBER: 60/354,409
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: 60/364,227
;  PRIOR FILING DATE: 2002-03-13
;  PRIOR APPLICATION NUMBER: 60/334,027
;  PRIOR FILING DATE: 2001-11-28
;  PRIOR APPLICATION NUMBER: 60/331,641
;  PRIOR FILING DATE: 2001-11-20
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 673
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 382
;   LENGTH: 522
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-287-226-382

  Query Match             93.6%;  Score 519.5;  DB 15;  Length 522;
  Best Local Similarity   76.4%;  Pred. No. 3.1e-52;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels   31;  Gaps    1;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKE----------------------- 36
              ||||||||||||||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKERWSFTMLPRLVWNSWAQGICLPRP 76

Qy         37 -------VLYYLGQYIMTKRLYDEKQQHIVHCSNDLLGDLFGVPSFSVKEHRKIYTMIYR 89
                   ||:|||||||||||||||||:||||||||||||||||||||||||||||
Db         77 PKVLDLQVLFYLGQYIMTKRLYDEKQQHIVYCSNDLLGDLFGVPSFSVKEHRKIYTMIYR 136

Qy         90 NLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||
Db        137 NLVVVNQQESSDSGTSVSEN 156


RESULT 14
US-09-956-425-6
; Sequence 6, Application US/09956425
; Patent No. US20020045192A1
; GENERAL INFORMATION:
;  APPLICANT: Kriwacki, Richard
;  APPLICANT:  Bothner, Brian
;  APPLICANT:  Lewis, William
;  TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and Method of Use Thereof
;  FILE REFERENCE: 1340/1/035
;  CURRENT APPLICATION NUMBER: US/09/956,425
;  CURRENT FILING DATE:  2001-09-19
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 489
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-956-425-6

  Query Match             87.5%;  Score 485.5;  DB 9;  Length 489;
  Best Local Similarity   86.2%;  Pred. No. 2.9e-48;
  Matches   94;  Conservative    9;  Mismatches    3;  Indels    3;  Gaps    1;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              |||||||||||||||||||||||||||| |||||||:::|:|||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQNDTYTMKEIIFYIGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||:|||||||||||||| ||||||| |:||   |||||:||:
Db         77 CSNDLLGDVFGVPSFSVKEHRKIYAMIYRNLVAVSQQ---DSGTSLSES 122


RESULT 15
US-09-966-724-4
; Sequence 4, Application US/09966724
; Publication No. US20040170971A1
;  GENERAL INFORMATION:
;       APPLICANT: THE JOHNS HOPKINS UNIVERSITY
;                  720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA
;       TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
;                           HUMAN TUMORS
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
;            STREET: 1001 G ST., N.W.
;            CITY: WASHINGTON
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20001-4597
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/966,724
;            FILING DATE: 01-Oct-2001
;            CLASSIFICATION: 435
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/044,619
;            FILING DATE: 2001-10-01
;            APPLICATION NUMBER: US 07/867.840
;            FILING DATE: 07-APR-1992
;       ATTORNEY/AGENT INFORMATION:
;            NAME: KAGAN, SARAH A.
;            REGISTRATION NUMBER: 32,141
;            REFERENCE/DOCKET NUMBER: 01107.40148
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-508-9100
;            TELEFAX: 202-508-9299
;            TELEX: 197430 BBMB UT
;   INFORMATION FOR SEQ ID NO: 4:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 489 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-966-724-4

  Query Match             87.5%;  Score 485.5;  DB 11;  Length 489;
  Best Local Similarity   86.2%;  Pred. No. 2.9e-48;
  Matches   94;  Conservative    9;  Mismatches    3;  Indels    3;  Gaps    1;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVH 60
              |||||||||||||||||||||||||||| |||||||:::|:|||||||||||||||||:
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQNDTYTMKEIIFYIGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
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Db         77 CSNDLLGDVFGVPSFSVKEHRKIYAMIYRNLVAVSQQ---DSGTSLSES 122
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Search completed: January 27, 2005, 18:23:06
Job time : 70.4 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:45:30 ; Search time 80.8 Seconds
(without alignments)
483.929 Million cell updates/sec

Title: US-10-822-254-12
Perfect score: 554
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	511	92.2	284	2	AAR75494	Aar75494 Human dou
2	511	92.2	284	2	AAR75397	Aar75397 Human dou
3	511	92.2	491	2	AAR42175	Aar42175 Human MDM
4	511	92.2	491	2	AAR76696	Aar76696 Human MDM
5	511	92.2	491	2	AAW07887	Aaw07887 Human MDM
6	511	92.2	491	2	AAW15463	Aaw15463 Human MDM
7	511	92.2	491	2	AAW13380	Aaw13380 Human MDM
8	511	92.2	491	2	AAW13600	Aaw13600 Murine do
9	511	92.2	491	2	AAW48241	Aaw48241 Human MDM
10	511	92.2	491	2	AAW57241	Aaw57241 Human MDM
11	511	92.2	491	2	AAW42879	Aaw42879 Amino aci
12	511	92.2	491	2	AAW42971	Aaw42971 Amino aci
13	511	92.2	491	2	AAW94304	Aaw94304 Human MDM
14	511	92.2	491	3	AAY96567	Aay96567 MDM2 onco
15	511	92.2	491	4	AAB48284	Aab48284 Human MDM
16	511	92.2	491	5	AAE22654	Aae22654 Human Rin
17	511	92.2	491	5	AAE22698	Aae22698 Human Rin
18	511	92.2	491	5	AAE25913	Aae25913 Human dou
19	511	92.2	491	5	AAO15376	Aao15376 Human Dm2
20	511	92.2	491	7	ADD21815	Add21815 Human mdm
21	511	92.2	491	7	ADE61562	Ade61562 Human Pro
22	511	92.2	491	8	ADL23893	Adl23893 Human E3
23	511	92.2	491	8	ADO52353	Ado52353 Human p53
24	511	92.2	491	8	ADP12593	Adp12593 Protein e
25	511	92.2	491	8	ADN71936	Adn71936 MDM2 prot
26	511	92.2	491	8	ADQ19417	Adq19417 Human sof
27	511	92.2	1171	4	AAU32421	Aau32421 Novel hum
28	494.5	89.3	216	3	AAB08846	Aab08846 A human M
29	485.5	87.6	522	7	ADJ95152	Adj95152 Novel NOV
30	485.5	87.6	522	7	ADJ95154	Adj95154 Novel NOV
31	451.5	81.5	489	2	AAR42176	Aar42176 Murine MD
32	451.5	81.5	489	2	AAR76697	Aar76697 Mouse MDM
33	451.5	81.5	489	2	AAW07888	Aaw07888 Murine MD
34	451.5	81.5	489	2	AAW15464	Aaw15464 Murine MD
35	451.5	81.5	489	2	AAW48242	Aaw48242 Mouse MDM
36	451.5	81.5	489	2	AAW57246	Aaw57246 Mouse MDM
37	451.5	81.5	489	2	AAW42997	Aaw42997 Amino aci
38	451.5	81.5	489	2	AAW42972	Aaw42972 Amino aci
39	451.5	81.5	489	2	AAW94305	Aaw94305 Mouse MDM
40	451.5	81.5	489	5	AAE25914	Aae25914 Mouse dou
41	451.5	81.5	489	5	ABB57099	Abb57099 Mouse isc
42	451.5	81.5	489	5	AAO15375	Aao15375 Mouse Dm2
43	451.5	81.5	489	7	ADD21816	Add21816 Mouse mdm
44	451.5	81.5	489	7	ADE61560	Ade61560 Rat Prote
45	329	59.4	227	2	AAR75495	Aar75495 Human dou

ALIGNMENTS

RESULT 1
AAR75494
ID AAR75494 standard; protein; 284 AA.
XX
AC AAR75494;
XX
DT 02-FEB-1996 (first entry)
XX
DE Human double minute 2 (hdm-2) antibody-binding region fragment 1.
XX
KW Human double minute gene 2; hdm-2; antibody binding region; antigen;
KW cancer; sarcoma; rhabdomyosarcoma; diagnosis; immunoassay.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1. .284
FT /note= "amino acids 1-284 of hdm-2 gene product"
XX
PN DE4339533-A1.
XX
PD 14-JUN-1995.
XX
PF 19-NOV-1993; 93DE-04339533.
XX
PR 19-NOV-1993; 93DE-04339533.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Zentgraf H, Klein R, Frey M, Martens R;
XX
DR WPI; 1995-216248/29.
DR N-PSDB; AAQ92515.
XX
PT Detection of human double minute gene 2 (hdm-2) antibodies - by
PT incubation with new hdm-2 or antibody-binding hdm-2 fragments; useful in
PT the detection of specific cancers.
XX
PS Claim 11; Fig 1; 12pp; German.
XX
CC Fragments contg. amino acids 1-284, 58-284 and 58-491 of the hdm-2 (human
CC double minute 2) gene product are claimed. The overlapping protein
CC fragments contain binding regions for hdm-2- specific antibodies and are
CC useful for identifying such antibodies in a claimed immunoassay method.
CC The presence of anti-hdm-2 antibodies is diagnostic of certain forms of
CC cancer, e.g. rhabdomyosarcoma
XX
SQ Sequence 284 AA;

```
  Query Match             92.2%;  Score 511;  DB 2;  Length 284;
  Best Local Similarity   94.5%;  Pred. No. 1.1e-53;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 2
AAR75397
ID   AAR75397 standard; protein; 284 AA.
XX
AC   AAR75397;
XX
DT   25-MAR-2003  (revised)
DT   25-JAN-1996  (first entry)
XX
DE   Human double minute 2 (hdm-2) antibody-binding region fragment 1.
XX
KW   Human double minute gene 2; hdm-2; antibody binding region; antigen;
KW   cancer; sarcoma; rhabdomyosarcoma; diagnosis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .284
FT                   /note= "amino acids 1-284 of hdm-2 gene product"
XX
PN   DE4345249-A1.
XX
PD   24-MAY-1995.
XX
PF   19-NOV-1993;   93DE-04345249.
XX
PR   19-NOV-1993;   93DE-04339533.
XX
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI   Zentgraf H,  Klein R,  Frey M,  Martens R;
XX
DR   WPI; 1995-195167/26.
DR   N-PSDB; AAQ87261.
XX
PT   New hdm-2 fragments contg. antibody binding region - used to detect
PT   specific antibodies for diagnosis of cancers, also new DNA sequences
PT   encoding them.
XX
PS   Claim 2; Fig 1; 11pp; German.
XX
CC   Fragments contg. amino acids 1-284, 58-284 and 58-491 of the hdm-2 (human
CC   double minute 2) gene product are claimed. The overlapping protein
CC   fragments contain binding regions for hdm-2- specific antibodies and are
CC   useful for identifying such antibodies. The presence of anti-hdm-2
CC   antibodies is diagnostic of certain forms of cancer, e.g.
CC   rhabdomyosarcoma. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 284 AA;

  Query Match             92.2%;  Score 511;  DB 2;  Length 284;
  Best Local Similarity   94.5%;  Pred. No. 1.1e-53;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 3
AAR42175
ID   AAR42175 standard; protein; 491 AA.
XX
AC   AAR42175;
XX
DT   25-MAR-2003  (revised)
DT   05-MAY-1994  (first entry)
XX
DE   Human MDM2.
XX
KW   p53 gene; tumour suppressor gene; regulation; cellular proliferation;
KW   cellular transformation; carcinoma; human; tumour; MDM2; inhibition;
KW   gene amplification.
XX
OS   Homo sapiens.
XX
PN   WO9320238-A2.
XX
PD   14-OCT-1993.
XX
PF   07-APR-1993;   93WO-US003199.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Burrell M,  Hill DE,  Kinzler KW,  Vogelstein B;
XX
DR   WPI; 1993-336944/42.
DR   N-PSDB; AAQ49891.
XX
PT   Diagnosing neoplasia from amplification of MDM2 gene - or elevated gene
PT   expression, also new DNA, MDM2 protein, antibodies and treatment of
PT   sarcoma by inhibiting MDM2 expression.
XX
PS   Claim 19; Fig 1; 75pp; English.
XX
CC   This sequence is encoded by the MDM2 gene. Amplification of the MDM2 gene
CC   is diagnostic of neoplasia or the potential for neoplasia. The protein
CC   encoded by this gene interacts with the product of the p53 gene. p53 is a
CC   tumour suppressor gene and encodes a protein which appears to be a member
CC   of a group of proteins which regulate normal cellular proliferation and
CC   suppression of cellular transformation. Inactivation of the p53 gene has
CC   been implicated in the formation, or progression of a wide variety of
CC   carcinoma. Polypeptides containing at least amino acids 13-41 of p53, or
CC   the DNA encoding these, may be used to inhibit the growth of tumour cells
CC   containing MDM2 gene amplification. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 491 AA;

  Query Match             92.2%;  Score 511;  DB 2;  Length 491;
  Best Local Similarity   94.5%;  Pred. No. 2.3e-53;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
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Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 4
AAR76696
ID   AAR76696 standard; protein; 491 AA.
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XX
AC   AAR76696;
XX
DT   16-OCT-2003  (revised)
DT   01-NOV-1995  (first entry)
XX
DE   Human MDM2 protein.
XX
KW   MDM2; sarcoma; diagnostic; DNA probe.
XX
OS   Homo sapiens; (cell line CaCo-2).
XX
PN   US5420263-A.
XX
PD   30-MAY-1995.
XX
PF   07-APR-1993;   93US-00044619.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Vogelstein B,  Kinzler KW;
XX
DR   WPI; 1995-206312/27.
DR   N-PSDB; AAQ94589.
XX
PT   New human MDM2 cDNA - used to develop prods. for use in the diagnosis and
PT   treatment of tumours.
XX
PS   Claim 1; Col 23-26; 34pp; English.
XX
CC   The human MDM2 gene is genetically altered (i.e. amplified) in human
CC   tumour cells. The human MDM2 protein binds to human p53 and allows the
CC   cell to escape from p53-regulated growth. Detecting that the gene has
CC   become amplified or detecting increased gene product expression (using
CC   probes, proteins, antibodies and inhibitors) allows diagnosis and therapy
CC   of cancers such as colorectal carcinoma, lung cancer and chronic
CC   myelogenous leukaemia. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ   Sequence 491 AA;

  Query Match             92.2%;  Score 511;  DB 2;  Length 491;
  Best Local Similarity   94.5%;  Pred. No. 2.3e-53;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 5
AAW07887
ID   AAW07887 standard; protein; 491 AA.
XX
AC   AAW07887;
XX
DT   25-MAR-2003  (revised)
DT   28-JAN-1997  (first entry)
XX
DE   Human MDM-2, involved in tumour-development.
XX
KW   p53; MDM-2; binding-inhibitor; identification; tumour; cancer; neoplasia;
KW   antibody fusion protein; therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   166. .169
FT                   /label= phosphorylation_site
FT                   /note= "potential casein kinase II phosphorylation site"
FT   Binding-site    181. .185
FT                   /label= nuclear_localisation_signal
FT   Modified-site   192. .195
FT                   /label= phosphorylation_site
FT                   /note= "potential casein kinase II phosphorylation site"
FT   Domain          223. .274
FT                   /label= acid_activation_domain
FT   Modified-site   269. .272
FT                   /label= phosphorylation_site
FT                   /note= "potential casein kinase II phosphorylation site"
FT   Modified-site   290. .293
FT                   /label= phosphorylation_site
FT                   /note= "potential casein kinase II phosphorylation site"
FT   Domain          305. .322
FT                   /label= metal_binding_site
FT   Domain          461. .478
FT                   /label= metal_binding_site
XX
PN   US5550023-A.
XX
PD   27-AUG-1996.
XX
PF   18-MAY-1994;   94US-00245500.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
PR   07-APR-1993;   93US-00044619.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Vogelstein B,  Kinzler KW;
XX
DR   WPI; 1996-401591/40.
DR   N-PSDB; AAT45151.
XX
PT   Identification of cpds. interfering with human MDM2/p53 binding - useful
PT   as therapeutic agents to treat human neoplastic cells.
XX
PS   Claim 26; Col 25-28; 36pp; English.
XX
CC   AAW07887 represents human MDM-2 derived from a human colon carcinoma cell
CC   line, CaCo-2, cDNA library. The MDM-2 protein is used in a method for
CC   identifying compounds that interfere with the binding of p53 and MDM-2.
CC   In binding the p53 protein, the MDM-2 protein releases a cell from p53-
CC   regulated growth, allowing cancers to develop. Therefore compounds
CC   identified as interfering with the binding of MDM-2 to p53 are
CC   potentially useful in the treatment of human neoplastic cells. In the
CC   method pref. one or both of the proteins is a fusion protein esp. with an
CC   antibody or antibody fragment which aids separation and identification.
CC   (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 491 AA;

  Query Match             92.2%;  Score 511;  DB 2;  Length 491;
  Best Local Similarity   94.5%;  Pred. No. 2.3e-53;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 6
AAW15463
ID   AAW15463 standard; protein; 491 AA.
XX
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```
AC   AAW15463;
XX
DT   25-MAR-2003  (revised)
DT   18-JUN-1997  (first entry)
XX
DE   Human MDM2.
XX
KW   Human; MDM2 protein; antibody; detection; cancer; diagnosis;
KW   p53-regulated growth.
XX
OS   Homo sapiens.
XX
PN   US5618921-A.
XX
PD   08-APR-1997.
XX
PF   17-FEB-1995;   95US-00390479.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
PR   07-APR-1993;   93US-00044619.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Vogelstein B,  Kinzler KW,  Burrell M,  Hill DE;
XX
DR   WPI; 1997-225474/20.
DR   N-PSDB; AAT66410.
XX
PT   Antibodies specific for human MDM2 protein - for diagnosis of cancer.
XX
PS   Claim 1; Col 19-24; 35pp; English.
XX
CC   This sequence represents the human MDM2 protein. Antibodies that
CC   specifically bind to human MDM2 protein may be used for detecting
CC   elevated expression of the MDM2 gene in a human tissue or body fluid
CC   sample, esp. for cancer diagnosis. The antibodies may be used to
CC   interfere with the binding of p53 to MDM2. Elevated levels of MDM2 appear
CC   to sequester p53 and allow the cell to escape from p53-regulated growth.
CC   (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 491 AA;

  Query Match             92.2%;  Score 511;  DB 2;  Length 491;
  Best Local Similarity   94.5%;  Pred. No. 2.3e-53;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 7
AAW13380
ID   AAW13380 standard; protein; 491 AA.
XX
AC   AAW13380;
XX
DT   25-MAR-2003  (revised)
DT   05-JUN-1997  (first entry)
XX
DE   Human MDM2 protein.
XX
KW   Human; MDM2; CaCo-2; colonic; carcinoma; probe; detection; amplification;
KW   elevation; expression; diagnosis; neoplasia; neoplastic transformation;
KW   sarcoma; colorectal; lung cancer; chronic myelogenous leukaemia.
XX
OS   Homo sapiens.
XX
PN   US5606044-A.
XX
PD   25-FEB-1997.
XX
PF   17-FEB-1995;   95US-00390546.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
PR   07-APR-1993;   93US-00044619.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Kinzler KW,  Vogelstein B,  Hill DE,  Burrell M;
XX
DR   WPI; 1997-153623/14.
DR   N-PSDB; AAT62065.
XX
PT   Detection of amplification of human MDM2 gene - useful for diagnosis of
PT   neoplasia or potential neoplastic transformation.
XX
PS   Example 1; Col 21-24; 35pp; English.
XX
CC   The present sequence is the human MDM2 protein, the cDNA for which was
CC   isolated from a human CaCo-2 colonic carcinoma cell cDNA library using a
CC   murine MDM2 cDNA probe. The MDM2 cDNA can be used as a probe to detect
CC   the amplification or elevated expression of a human MDM2 gene, which is
CC   diagnostic of neoplasia or the potential for neoplastic transformation,
CC   useful for the detection of, e.g. sarcomas, colorectal carcinoma, lung
CC   cancer and chronic myelogenous leukaemia. (Updated on 25-MAR-2003 to
CC   correct PF field.)
XX
SQ   Sequence 491 AA;

  Query Match             92.2%;  Score 511;  DB 2;  Length 491;
  Best Local Similarity   94.5%;  Pred. No. 2.3e-53;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 8
AAW13600
ID   AAW13600 standard; protein; 491 AA.
XX
AC   AAW13600;
XX
DT   16-JAN-1998  (first entry)
XX
DE   Murine double minute 2 protein sequence.
XX
KW   Mouse; Mdm2; murine double minute; phosphoprotein; binding; modulation;
KW   tumour suppressor; p53; oncogene; cell cycle arrest; p107; antagonist;
KW   inhibition; transcription factor; adenocarcinoma; colon; cancer; breast;
KW   lung; stomach; myeloid leukaemia; lymphoma; hyperproliferative;
KW   restenosis.
XX
OS   Mus musculus.
XX
PN   WO9709343-A2.
XX
PD   13-MAR-1997.
XX
PF   02-SEP-1996;   96WO-FR001340.
XX
PR   04-SEP-1995;   95FR-00010331.
XX
PA   (RHON ) RHONE POULENC RORER SA.
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PA (INRM) INST NAT SANTE & RECH MEDICALE.
XX
PI Tocque B, Dubs-Poterszman M, Wasylyk B;
XX
DR WPI; 1997-192837/17.
DR N-PSDB; AAT61637.
XX
PT Treating cancer with antagonist of oncogenic activity of protein Mdm2 -
PT or nucleic acid encoding an antagonist, also viral vectors contg. this
PT nucleic acid.
XX
PS Claim 2; Page 26-30; 43pp; French.
XX
CC This is the amino acid sequence of the mouse Mdm2 (murine double minute-
CC 2) protein, a 90 kD phosphoprotein which binds and modulates the activity
CC of the tumour suppressor protein p53. It has now been shown that the mdm2
CC protein itself has oncogenic properties, especially in a p53-null
CC background. Mdm2 is observed to unblock cell cycle arrest in G1 caused by
CC over-expression of the p107 protein. This is especially done by the
CC region covering amino acid 1-134. The invention therefore relates to
CC antagonists able to inhibit the oncogenic activity of mdm2. These include
CC fragments of the p53 protein, especially amino acids 1-52, 1-41, 6-41, 16
CC -25 or 18-23 (AAW13602-6), or fragments of transcription factors e.g.
CC TFII, TBP or TAF250, which bind amino acids 1-134 of mdm2. Other
CC inhibitors include compounds which disrupt binding to region 135-491 of
CC mdm2, e.g. Rb, L5 or the transcription factor E2F. The antagonists are
CC used to treat e.g. adenocarcinoma of the colon; cancer of the breast,
CC lung or stomach; myeloid leukaemia; B cell lymphoma, or other
CC hyperproliferative conditions such as restenosis
XX
SQ Sequence 491 AA;

Query Match 92.2%; Score 511; DB 2; Length 491;
Best Local Similarity 94.5%; Pred. No. 2.3e-53;
Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy 61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN
Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125

RESULT 9
AAW48241
ID AAW48241 standard; protein; 491 AA.
XX
AC AAW48241;
XX
DT 18-JUN-1998 (first entry)
XX
DE Human MDM2.
XX
KW Human; MDM2; hMDM2; tumour; cancer; diagnosis; neoplastic disease;
KW sarcoma; liposarcoma; malignant fibrous histiocytoma; osteosarcoma.
XX
OS Homo sapiens.
XX
PN US5736338-A.
XX
PD 07-APR-1998.
XX
PF 17-FEB-1995; 95US-00390517.
XX
PR 07-APR-1992; 92US-00867840.
PR 23-JUN-1992; 92US-00903103.
PR 07-APR-1993; 93US-00044619.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Vogelstein B, Kinzler KW, Hill DE, Burrell M;
XX
DR WPI; 1998-239206/21.
DR N-PSDB; AAV20549.
XX
PT Cancer diagnosis - by determination of MDM2 protein.
XX
PS Claim 1; Col 25-28; 35pp; English.
XX
CC The present sequence represents human MDM2 (hMDM2) which is used in the
CC method of the present invention. The present invention describes a method
CC for diagnosing a neoplastic disease caused by overexpression of MDM2
CC protein. The method comprises detecting an elevated cellular amount of
CC this protein. The method is useful for the diagnosis of sarcoma,
CC especially liposarcoma, malignant fibrous histiocytoma or osteosarcoma
XX
SQ Sequence 491 AA;

Query Match 92.2%; Score 511; DB 2; Length 491;
Best Local Similarity 94.5%; Pred. No. 2.3e-53;
Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy 61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN
Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125

RESULT 10
AAW57241
ID AAW57241 standard; protein; 491 AA.
XX
AC AAW57241;
XX
DT 10-AUG-1998 (first entry)
XX
DE Human MDM2 protein.
XX
KW Human; p53; MDM2; tumour; growth inhibition; amplification;
KW malignant fibrous histiocytoma; liposarcoma.
XX
OS Homo sapiens.
XX
PN US5756455-A.
XX
PD 26-MAY-1998.
XX
PF 17-FEB-1995; 95US-00390515.
XX
PR 07-APR-1992; 92US-00867840.
PR 23-JUN-1992; 92US-00903103.
PR 07-APR-1993; 93US-00044619.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Vogelstein B, Kinzler KW;
XX
DR WPI; 1998-321574/28.
DR N-PSDB; AAV28876.
XX
PT Inhibiting growth of tumour cells having MDM2 gene amplification - with
PT p53 protein fragment.
XX
PS Claim 1; Col 23-28; 40pp; English.
XX
CC A method has been developed for inhibiting the growth of tumour cells
CC containing a human MDM2 gene amplification. The method comprises treating
CC the tumour cells with a DNA molecule that expresses a polypeptide capable
CC of binding to human MDM2 protein. The present sequence represents human
CC MDM2 protein. The present invention describes three preferred
CC polypeptides for binding human MDM2: (1) the polypeptide comprises amino

CC acids 1-50 of p53 (see AAW57240); (2) the polypeptide comprises amino
CC acids 13-41 of p53 (see AAW57240) and at least none additional p53
CC residues on the N- or C-terminal side, provided that the polypeptide
CC lacks the homooligomerisation domain of p53; (3) the polypeptide
CC comprises amino acids 13-41 of p53 (see AAW57241) and at least nine
CC additional p53 residues on the N- or C-terminal side, provided that the
CC polypeptide lacks amino acids 138-393 of p53. Some malignant fibrous
CC histiocytomas and liposarcomas have an MDM2 gene amplification, so
CC detection of increased expression of MDM2 gene products indicates
CC tumourigenesis
XX
SQ Sequence 491 AA;

Query Match 92.2%; Score 511; DB 2; Length 491;
Best Local Similarity 94.5%; Pred. No. 2.3e-53;
Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy 61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125

RESULT 11
AAW42879
ID AAW42879 standard; protein; 491 AA.
XX
AC AAW42879;
XX
DT 30-APR-1998 (first entry)
XX
DE Amino acid sequence of human MDM2.
XX
KW MDM2; tumour; diagnosis; neoplasia; DNA binding protein; p53 polypeptide;
KW binding; tumour cell; p53-regulated growth; inhibition;
KW anti-cancer agent.
XX
OS Homo sapiens.
XX
PN US5708136-A.
XX
PD 13-JAN-1998.
XX
PF 17-FEB-1995; 95US-00390516.
XX
PR 07-APR-1992; 92US-00867840.
PR 23-JUN-1992; 92US-00903103.
PR 07-APR-1993; 93US-00044619.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Vogelstein B, Kinzler KW, Burrell M, Hill DE;
XX
DR WPI; 1998-100408/09.
XX
PT Human MDM2 binding polypeptide - comprises fragments of p53, useful in re
PT -establishing p53-regulated growth control in cells over-expressing MDM2.
XX
PS Disclosure; Col 23-28; 41pp; English.
XX
CC The present sequence represents human MDM2. The MDM2 gene is amplified in
CC some human tumours. The amplification of this gene is diagnostic of
CC neoplasia or its potential. It is speculated that the MDM2 protein is a
CC potential DNA binding protein that functions in the modulation of
CC expression of other genes and, when present in excess, inteferes with
CC normal constraints on cell growth. A cell containing three recombinant
CC DNA constructs was produced. These constructs encode an MDM2 protein
CC fused to a sequence-specific DNA binding domain, a p53 polypeptide fused
CC to a transcriptional activation domain, and a reporter gene downstream
CC from a DNA element which is recognised by the sequence-specific DNA-
CC binding domain. The cell is used to identify a compound which interferes
CC with the binding of MDM2 and p53. Since MDM2 is overexpressed in tumour
CC cells and since binding of MDM2 to p53 appears to allow tumour cells to
CC escape from p53-regulated growth, compounds that inhibit such binding
CC would be useful as anti-cancer agents
XX
SQ Sequence 491 AA;

Query Match 92.2%; Score 511; DB 2; Length 491;
Best Local Similarity 94.5%; Pred. No. 2.3e-53;
Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy 61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125

RESULT 12
AAW42971
ID AAW42971 standard; protein; 491 AA.
XX
AC AAW42971;
XX
DT 29-APR-1998 (first entry)
XX
DE Amino acid sequence of human MDM2.
XX
KW MDM2; tumour; diagnosis; neoplasia; DNA binding protein; p53 polypeptide;
KW binding; tumour cell; p53-regulated growth; inhibition;
KW anti-cancer agent.
XX
OS Homo sapiens.
XX
PN US5702903-A.
XX
PD 30-DEC-1997.
XX
PF 13-NOV-1995; 95US-00557393.
XX
PR 07-APR-1992; 92US-00867840.
PR 23-JUN-1992; 92US-00903103.
PR 07-APR-1993; 93US-00044619.
PR 18-MAY-1994; 94US-00245500.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Vogelstein B, Kinzler KW;
XX
DR WPI; 1998-076411/07.
DR N-PSDB; AAV03607.
XX
PT Cell containing reporter construct containing human MDM2 and p53 genes -
PT for identifying compounds that interfere with binding of human MDM2 to
PT human p53, useful as anti-cancer agents.
XX
PS Disclosure; Coulmns 22-28; 37pp; English.
XX
CC The present sequence represents human MDM2. The MDM2 gene is amplified in
CC some human tumours. The amplification of this gene is diagnostic of
CC neoplasia or its potential. It is speculated that the MDM2 protein is a
CC potential DNA binding protein that functions in the modulation of
CC expression of other genes and, when present in excess, inteferes with
CC normal constraints on cell growth. A cell containing three recombinant
CC DNA constructs was produced. These constructs encode an MDM2 protein
CC fused to a sequence-specific DNA binding domain, a p53 polypeptide fused
CC to a transcriptional activation domain, and a reporter gene downstream
CC from a DNA element which is recognised by the sequence-specific DNA-
CC binding domain. The cell is used to identify a compound which interferes
CC with the binding of MDM2 and p53. Since MDM2 is overexpressed in tumour

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CC   cells and since binding of MDM2 to p53 appears to allow tumour cells to
CC   escape from p53-regulated growth, compounds that inhibit such binding
CC   would be useful as anti-cancer agents
XX
SQ   Sequence 491 AA;

  Query Match             92.2%;  Score 511;  DB 2;  Length 491;
  Best Local Similarity   94.5%;  Pred. No. 2.3e-53;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 13
AAW94304
ID   AAW94304 standard; protein; 491 AA.
XX
AC   AAW94304;
XX
DT   13-APR-1999  (first entry)
XX
DE   Human MDM2.
XX
KW   Human; MDM2; p53; tumourigenesis; growth regulation; diagnosis;
KW   malignant fibrous histocytoma; MFH; liposarcoma.
XX
OS   Homo sapiens.
XX
PN   US5858976-A.
XX
PD   12-JAN-1999.
XX
PF   14-FEB-1997;   97US-00801718.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
PR   07-APR-1993;   93US-00044619.
PR   17-FEB-1995;   95US-00390515.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Kinzler KW,  Vogelstein B;
XX
DR   WPI; 1999-152105/13.
DR   N-PSDB; AAX03947.
XX
PT   Inhibiting growth of tumour cells having MDM2 gene amplification - with
PT   MDM2-binding p53 fragment.
XX
PS   Claim 1; Col 23-28; 41pp; English.
XX
CC   The present invention describes: (1) a method for inhibiting the growth
CC   of tumour cells which contain a human MDM2 gene amplification, comprising
CC   administering to the cells a DNA molecule that expresses a polypeptide
CC   consisting of a portion of p53 i.e. amino acids 13-41 of the 64 amino
CC   acid sequence given in AAW94303, the polypeptide being capable of binding
CC   to human MDM2 (the present sequence); (2) a method as in (1) where the
CC   polypeptide lacks the homo-oligomerisation domain of p53; and (3) a
CC   method as in (1) where the polypeptide lacks amino acids 138-393 of p53.
CC   The method is useful for treating the following tumour types which have a
CC   MDM2 gene amplification: M-7 malignant fibrous histocytoma (MFH), M-20
CC   MFH, L-9 liposarcoma, KL7 liposarcoma, KL28 liposarcoma, KL30
CC   liposarcoma, and OSA-CL MFH
XX
SQ   Sequence 491 AA;

  Query Match             92.2%;  Score 511;  DB 2;  Length 491;
  Best Local Similarity   94.5%;  Pred. No. 2.3e-53;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 14
AAY96567
ID   AAY96567 standard; protein; 491 AA.
XX
AC   AAY96567;
XX
DT   12-SEP-2000  (first entry)
XX
DE   MDM2 oncoprotein.
XX
KW   hEST2; telomerase; catalytic subunit; reverse transcriptase; life-span;
KW   retinoblastoma; p53; tumour suppressor; inhibitor; arteriosclerosis;
KW   proliferation; immortal; tumour therapy; macular degeneration; activator;
KW   INK4; MDM2; oncoprotein.
XX
OS   Homo sapiens.
XX
PN   WO200031238-A2.
XX
PD   02-JUN-2000.
XX
PF   24-NOV-1999;   99WO-US027907.
XX
PR   25-NOV-1998;   98US-0109891P.
PR   17-FEB-1999;   99US-0120549P.
XX
PA   (GENE-) GENETICA INC.
XX
PI   Hannon GJ,  Beach DH;
XX
DR   WPI; 2000-400055/34.
DR   N-PSDB; AAA29389.
XX
PT   New method for increasing the proliferative capacity of cell lines
PT   comprises administering agents reversibly activating telomerase activity
PT   and reversibly inactivating Rb/INk4 and/or p53 pathways useful in
PT   treating age related diseases.
XX
PS   Claim 5; Page 120; 123pp; English.
XX
CC   The invention concerns methods and reagents for extending the life-span,
CC   e.g. the number of mitotic divisions, of a cell. The method relies on
CC   activation of a telomerase activity and inhibition of one or both of a
CC   retinoblastoma (Rb)/INK4 pathway or a p53 pathway. Phosphorylation of Rb
CC   by cyclin-dependent kinases, cdk4 and cdk6, releases the cells into the
CC   division cycle. Binding of INK4 family members, e.g. the tumour
CC   suppressor p16INK4a, inhibits kinase activity and results in growth
CC   arrest. Rb inactivators can selectively and reversibly inactivate an
CC   Rb/INK4 pathway, especially an Rb/p16INK4a pathway. The oncoprotein MDM2
CC   is a cellular inhibitor of Rb/E2F function and the p53 tumour suppressor
CC   and can also be used in the methods. Other molecules which can be used
CC   include cdk4 or cdk6 mutants. In particular, a cdk4 mutant is one which
CC   differs from at one or more of residues K22, R24, H95 and/or D97.
CC   Additional constructs include a papilloma virus E7 protein, or other
CC   viral oncoprotein which bypasses Rb and/or p53. Antisense constructs of
CC   the Rb and p16INK4a genes may also be used. The methods are useful for
CC   increasing the proliferative capacity of cells. The cells are
CC   subsequently of use in pharmaceutical and cosmetic preparations used to
CC   treat conditions related to (premature) ageing, e.g. macular degeneration
CC   and arteriosclerosis. The cells can also be used to replace tumour cell
CC   lines in vitro and for studies on biochemical and physiological aspects
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CC   of growth and differentiation. Long lived (immortal) cells could also be
CC   of use in the production of normal or genetically engineered
CC   biotechnology products
XX
SQ   Sequence 491 AA;

  Query Match             92.2%;  Score 511;  DB 3;  Length 491;
  Best Local Similarity   94.5%;  Pred. No. 2.3e-53;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 15
AAB48284
ID   AAB48284 standard; protein; 491 AA.
XX
AC   AAB48284;
XX
DT   02-APR-2001  (first entry)
XX
DE   Human MDM2 protein.
XX
KW   S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF;
KW   CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;
KW   Bad; Bcl-2; tumour; cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO200075184-A1.
XX
PD   14-DEC-2000.
XX
PF   05-JUN-2000; 2000WO-US015449.
XX
PR   04-JUN-1999;   99US-0137494P.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Zhang H,  Tsvetkov LM,  Kondo T;
XX
DR   WPI; 2001-061703/07.
DR   N-PSDB; AAC84596.
XX
PT   Modulating polypeptide levels in a cell, diagnosing and treating tumor,
PT   involves altering levels of proteins such as S-phase kinase associated
PT   proteins 1, 2 and cullin/CDC53 proteins.
XX
PS   Claim 5; Page 93-95; 162pp; English.
XX
CC   The invention relates to methods of altering the polypeptide levels in a
CC   cell, using proteins selected from S-phase kinase associated proteins 1
CC   and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the
CC   cullin/ CDC53 family of proteins). The method is useful for altering the
CC   level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2
CC   polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for
CC   detecting tumours, and in monitoring tumor treatment in a mammal. Agents
CC   that modulate interactions between SKP and target proteins are useful for
CC   treating tumours
XX
SQ   Sequence 491 AA;

  Query Match             92.2%;  Score 511;  DB 4;  Length 491;
  Best Local Similarity   94.5%;  Pred. No. 2.3e-53;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


Search completed: January 27, 2005, 18:06:16
Job time : 80.8 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:52:56 ; Search time 19.8 Seconds
(without alignments)
529.678 Million cell updates/sec

Title: US-10-822-254-12
Perfect score: 554
Sequence: 1 SQIPASEQETKVRPKPKLLK.....NLVVVNQQESSDSGTSVSEN 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	511	92.2	491	1	S24354	p53-binding protei
2	451.5	81.5	489	2	S15349	mdm2 protein - mou
3	278.5	50.3	489	2	S71955	MDM2-like p53-bind
4	77.5	14.0	709	2	E64213	DNA topoisomerase
5	76.5	13.8	337	2	T19592	hypothetical prote
6	73	13.2	1751	2	A45604	major blood-stage
7	72	13.0	755	2	S58718	probable nuclear p
8	71.5	12.9	244	2	D71608	hypothetical prote
9	71.5	12.9	840	2	H96635	unknown protein, 7
10	71	12.8	838	2	I45557	eyeless, long form
11	70.5	12.7	223	2	C69215	conserved hypothet
12	70.5	12.7	525	2	T15185	hypothetical prote
13	70	12.6	215	2	S28062	homeotic protein g
14	70	12.6	337	1	ZHBPG4	gene H protein - p
15	69	12.5	187	2	S70186	21K protein - Shig
16	69	12.5	206	1	XUBYMC	methylated-DNA-[pr
17	69	12.5	413	2	E83950	processing protein
18	69	12.5	1233	1	G71612	novel serine/threo
19	68.5	12.4	425	2	T50184	mammalian swi/snf
20	68.5	12.4	636	2	H96666	probable phytochro
21	68.5	12.4	882	2	S57704	hypothetical prote
22	68.5	12.4	1292	2	F64237	DNA-directed RNA p
23	68	12.3	1098	2	S38100	hypothetical prote
24	67.5	12.2	245	2	F71889	hypothetical prote
25	67.5	12.2	263	2	AB2559	transposase all806
26	67.5	12.2	319	2	A42277	traA protein - Ent
27	67.5	12.2	353	2	D69001	conserved hypothet
28	67.5	12.2	446	2	S35524	telomere-binding p
29	67.5	12.2	600	2	H81733	DNA primase TC0175
30	67	12.1	286	2	B97743	exodeoxyribonuclea
31	67	12.1	418	2	B57511	interleukin-1 beta
32	67	12.1	683	2	T38254	serine/threonine-s
33	67	12.1	685	1	SXBPT4	NAD+-protein ADP-r
34	67	12.1	698	1	S31630	NAD+-protein ADP-r
35	67	12.1	698	1	S31714	NAD+-protein ADP-r
36	66.5	12.0	467	2	T25848	hypothetical prote
37	66.5	12.0	928	1	RBHU	retinoblastoma-ass
38	66	11.9	146	2	G71940	hypothetical prote
39	66	11.9	170	2	T31967	hypothetical prote
40	66	11.9	258	2	A64000	hypothetical prote
41	66	11.9	303	2	B95101	1-phosphofructokin
42	66	11.9	303	2	C97969	1-phosphofructokin
43	66	11.9	374	2	AD1970	serine/threonine k
44	66	11.9	425	2	C97035	uncharacterized pr
45	66	11.9	456	2	AG3471	beta-alanine-pyruv

ALIGNMENTS

RESULT 1
S24354
p53-binding protein mdm2 - human
N;Alternate names: mdm-2 oncogene; mouse double minute 2 homolog; p53-associated phospho
N;Contains: p53-binding protein mdm2, splice form A
C;Species: Homo sapiens (man)
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C;Accession: S24354; S57338; G02026
R;Oliner, J.D.; Kinzler, K.W.; Meltzer, P.S.; George, D.L.; Vogelstein, B.
Nature 358, 80-83, 1992
A;Title: Amplification of a gene encoding a p53-associated protein in human sarcomas.
A;Reference number: S24354; MUID:92310576; PMID:1614537
A;Accession: S24354
A;Molecule type: mRNA
A;Residues: 1-491 <OLI>
A;Cross-references: EMBL:Z12020; NID:g35211; PIDN:CAA78055.1; PID:g35212
R;Zauberman, A.; Flusberg, D.; Haupt, Y.; Barak, Y.; Oren, M.
Nucleic Acids Res. 23, 2584-2592, 1995
A;Title: A functional p53-responsive intronic promoter is contained within the human mdm
A;Reference number: S57338; MUID:95380270; PMID:7651818
A;Accession: S57338
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-16,'P',18-24 <ZAU>
A;Cross-references: EMBL:U28935; NID:g904033; PIDN:AAA82237.1; PID:g904034
R;Lunec, J.
submitted to the EMBL Data Library, August 1995
A;Description: Multiple alternate spliced mdm2 transcripts with loss of p53 binding doma
A;Reference number: G09070
A;Accession: G02026
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-27,223-491 <LUN>
A;Cross-references: EMBL:U33199; NID:g992676; PIDN:AAA75514.1; PID:g992677
A;Experimental source: splice form A
C;Genetics:
A;Gene: GDB:MDM2
A;Cross-references: GDB:250456; OMIM:164785
A;Map position: 12q14.3-12q15
C;Superfamily: human p53-binding protein mdm2
C;Keywords: alternative splicing; oncogene; phosphoprotein
F;1-491/Product: p53-binding protein mdm-2 #status predicted <MAT1>
F;1-27,223-491/Product: p53-binding protein mdm-2, splice form A #status predicted <MAT2

Query Match 92.2%; Score 511; DB 1; Length 491;
Best Local Similarity 94.5%; Pred. No. 8.3e-43;
Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              ||||||||||  |||||  ||||||||||||||||||||  ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76
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Qy          61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
               |||| ||||||| ||||||||||||||||||||||||||||||||||||
Db          77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 2
S15349
mdm2 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S15349
R;Fakharzadeh, S.S.; Trusko, S.P.; George, D.L.
EMBO J. 10, 1565-1569, 1991
A;Title: Tumorigenic potential associated with enhanced expression of a gene that is amp
A;Reference number: S15349; MUID:91224107; PMID:2026149
A;Accession: S15349
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-489 <FAK>
A;Cross-references: UNIPROT:P23804; EMBL:X58876; NID:g53038; PIDN:CAA41684.1; PID:g53039
C;Genetics:
A;Gene: mdm2
C;Superfamily: human p53-binding protein mdm2

  Query Match             81.5%;  Score 451.5;  DB 2;  Length 489;
  Best Local Similarity   82.6%;  Pred. No. 6.3e-37;
  Matches   90;  Conservative    7;  Mismatches    9;  Indels    3;  Gaps    1;

Qy           1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
               |||||||||| ||||| |||||||||| |||||||:: |:||||||||||||||||||
Db          17 SQIPASEQETLVRPKPLLLKLLKSVGAQNDTYTMKEIIFYIGQYIMTKRLYDEKQQHIVY 76

Qy          61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
               |||| |||:||| |||||||||| ||||||| |:||   |||||:||:
Db          77 CSNDLLGDVFGVPSFSVKEHRKIYAMIYRNLVAVSQQ---DSGTSLSES 122


RESULT 3
S71955
MDM2-like p53-binding protein MDMX - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
C;Accession: S71955
R;Shvarts, A.; Steegenga, W.T.; Riteco, N.; van Laar, T.; Dekker, P.; Bazuine, M.; van H
EMBO J. 15, 5349-5357, 1996
A;Title: MDMX: a novel p53-binding protein with some functional properties of MDM2.
A;Reference number: S71955; MUID:97050840; PMID:8895579
A;Accession: S71955
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-489 <SHV>
A;Cross-references: UNIPROT:O35618; EMBL:AF007110; NID:g2253388; PIDN:AAB62927.1; PID:g2
C;Genetics:
A;Gene: MDMX
C;Function:
A;Description: inhibits transcription activation function of tumour suppressor protein p
C;Superfamily: human p53-binding protein mdm2

  Query Match             50.3%;  Score 278.5;  DB 2;  Length 489;
  Best Local Similarity   52.4%;  Pred. No. 8.2e-20;
  Matches   55;  Conservative   19;  Mismatches   20;  Indels   11;  Gaps    1;

Qy           5 ASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVKCSND 64
               :||| ::|||| :|||:| : ||| : :|||||:|||||||| |:|||:::||:| |  |
Db          20 SSEQISQVRPKLQLLKILHAAGAQGEVFTMKEVMHYLGQYIMVKQLYDQQEQHMVYCGGD 79

Qy          65 KLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
               |||| | :|||||:   :| |: :|||           || | |
Db          80 LLGDLLGCQSFSVKDPSPLYDMLRKNLV----------TSASNN 113


RESULT 4
E64213
DNA topoisomerase (EC 5.99.1.2) - Mycoplasma genitalium
N;Alternate names: type I DNA topoisomerase
C;Species: Mycoplasma genitalium
C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
C;Accession: E64213
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
, C.A.; Venter, J.C.
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200; MUID:96026346; PMID:7569993
A;Accession: E64213
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-709 <TIGR>
A;Cross-references: UNIPROT:P47368; GB:U39691; GB:L43967; NID:g1045794; PID:g1045802; TI
A;Experimental source: strain G-37
C;Genetics:
A;Genetic code: SGC3
C;Superfamily: DNA topoisomerase I
C;Keywords: isomerase

  Query Match             14.0%;  Score 77.5;  DB 2;  Length 709;
  Best Local Similarity   24.7%;  Pred. No. 9.5;
  Matches   24;  Conservative   17;  Mismatches   39;  Indels   17;  Gaps    3;

Qy          30 DTYTMKEVLHYLGQ----YIMTK--------RLYDE-----KQQHIVKCSNDKLGDLFGV 72
               |  | : :: :: |    |  :|         |||:|     | :  :  |  |:|| |
Db         424 DAKTSRTIVRFINQKNKFYTSSKSLLFDGYQRLYEEIKPNTKDELYIDLSKLKIGDKFSF 483

Qy          73 KSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
               :  || ||:      |    :: : | |: |   : |
Db         484 EKISVNEHKTNPPPRYTQASLIEELEKSNIGRPSTYN 520


RESULT 5
T19592
hypothetical protein C30H6.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19592
R;Mortimore, B.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19148
A;Accession: T19592
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-337 <WIL>
A;Cross-references: UNIPROT:O45279; EMBL:Z81044; PIDN:CAB02813.1; GSPDB:GN00022; CESP:C3
A;Experimental source: clone C30H6
C;Genetics:
A;Gene: CESP:C30H6.7
A;Map position: 4
A;Introns: 19/2; 85/3; 120/3; 166/3; 240/2; 286/2

  Query Match             13.8%;  Score 76.5;  DB 2;  Length 337;
  Best Local Similarity   26.6%;  Pred. No. 5.1;
  Matches   33;  Conservative   17;  Mismatches   33;  Indels   41;  Gaps    6;

Qy          14 PKPK-LLK--LLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVKCSNDKLGDLF 70
               || | :||  ::| | |:|    :| | |:          :  |: ||   | :|  |:|
Db          44 PKNKNILKGDVMKIVEAEK----LKPVAHH---------AHAPKETHIENKSIEKKSDIF 90

Qy          71 GVKSFSVKEHR-----KIYTMIYRNLVVVNQ-------------------QESSDSGTS 105
               |  : |:: |:       |  | : |    |                    |:   |||:
Db          91 GANNRSLRHHQDIPLSNIRATIAKRLTASKQQIPHEYQGVDVRIDDILALRQKLKKSGTA 150

Qy         106 VSEN 109
               || |
Db         151 VSLN 154


RESULT 6
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A45604
major blood-stage surface antigen Pv200 - Plasmodium vivax
C;Species: Plasmodium vivax
C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A45604
R;Gibson, H.L.; Tucker, J.E.; Kaslow, D.C.; Krettli, A.U.; Collins, W.E.; Kiefer, M.C.;
Mol. Biochem. Parasitol. 50, 325-333, 1992
A;Title: Structure and expression of the gene for Pv200, a major blood-stage surface ant
A;Reference number: A45604; MUID:92158013; PMID:1371329
A;Accession: A45604
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1751 <GIB>
A;Cross-references: UNIPROT:Q26194; GB:M75674; NID:g160608; PID:g457336
A;Note: sequence extracted from NCBI backbone (NCBIN:83591, NCBIP:83592)
C;Superfamily: major merozoite surface antigen
C;Keywords: surface antigen

  Query Match             13.2%;  Score 73;  DB 2;  Length 1751;
  Best Local Similarity   27.6%;  Pred. No. 74;
  Matches   35;  Conservative   20;  Mismatches   42;  Indels   30;  Gaps    7;

Qy          4 PASEQETKVRPKP---------KLLKLLKSVGA-QKDTY----TMKEVLHYLGQYIMTKR 49
              | |     | | |         |||  |||  |  |  :    |||: |  | ||    :
Db        816 PPSTPAAAVAPAPTMSKLEYLEKLLDFLKSAYACHKHIFVTNSTMKKEL--LDQY----K 869

Qy         50 LYDEKQQHIVKCSNDKLGDLFGVKS-----FSV-----KEHRKIYTMIYRNLVVVNQQES 99
              |  ::|  | :   |:|  || |::     :|:      | : :|  :|:  :| |  ::
Db        870 LNADEQNKINETKCDELDLLFNVQNNLPAMYSIYDSMSNELQNLYIELYQKEMVYNIYKN 929

Qy        100 SDSGTSV 106
              |:   :
Db        930 KDTDKKI 936


RESULT 7
S58718
probable nuclear protein YNL059c - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein N2430; protein YNL1620
C;Species: Saccharomyces cerevisiae
C;Date: 16-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C;Accession: S58718; S62987
R;Bergez, P.; Doignon, F.; Crouzet, M.
Yeast 11, 967-974, 1995
A;Title: The sequence of a 44 420 bp fragment located on the left arm of chromosome XIV
A;Reference number: S58711; MUID:96021608; PMID:8533472
A;Accession: S58718
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-755 <BER>
A;Cross-references: UNIPROT:P53946; EMBL:U12141; NID:g1314216; PIDN:AAA99652.1; PID:g994
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
R;Bergez, P.; Doignon, F.; Crouzet, M.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S62975
A;Accession: S62987
A;Molecule type: DNA
A;Residues: 1-755 <BEW>
A;Cross-references: EMBL:Z71335; NID:g1301931; PID:e239897; PID:g1301932; MIPS:YNL059c
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:ARP5
A;Cross-references: SGD:S0005004; MIPS:YNL059c
A;Map position: 14L

  Query Match             13.0%;  Score 72;  DB 2;  Length 755;
  Best Local Similarity   27.5%;  Pred. No. 36;
  Matches   25;  Conservative   16;  Mismatches   34;  Indels   16;  Gaps    4;

Qy          7 EQETKVR------PKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYD-EKQQHIV 59
              |  :|||       || |:| :|:: |    |     |: || | | :   :: : |    |:
Db        328 EYFSKVRDQLIDEPKKKVLSVLQNAGFD-DERDFKKYLHSLEQSLKKAQMVEAEDDSHLD 386

Qy         60 KCSNDKLGDLFGVKSFS--------VKEHRK 82
              : : ||    | :   :         :|| ||
Db        387 EMNEDKTAQKFDLLDIADEDLNEDQIKEKRK 417


RESULT 8
D71608
hypothetical protein PFB0690w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
C;Accession: D71608
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.,
.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743; PMID:9804551
A;Accession: D71608
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-244 <GAR>
A;Cross-references: UNIPROT:O96231; GB:AE001412; GB:AE001362; NID:g3845251; PIDN:AAC7192
A;Experimental source: clone 3D7
C;Genetics:
A;Gene: PFB0690w

  Query Match             12.9%;  Score 71.5;  DB 2;  Length 244;
  Best Local Similarity   23.8%;  Pred. No. 11;
  Matches   25;  Conservative   24;  Mismatches   47;  Indels    9;  Gaps    3;

Qy          6 SEQETKVRPKPKLLKLLKSVGAQKDTY-----TMKEVLHYLGQYIMTKRLYDEKQQHIV- 59
              |: : |   | ||   |||:      :      |::|::| : | : ||       ::|
Db         94 SDYKFKTETKSKLESKLKSLKDMNKIHKFEHDTLEELVHKMEQELETKMYIKNDIENIFN 153

Qy         60 KCSNDK---LGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSD 101
              :| | |   | |:   :    || :|    : : |::: |: : :
Db        154 ECINKKDEYLKDITQERISVFKERKKRQNQLQKLLLIMKQENNKN 198


RESULT 9
H96635
unknown protein, 73054-77165 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: H96635
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: H96635
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-840 <STO>
A;Cross-references: UNIPROT:Q9C951; GB:AE005173; NID:g6751691; PIDN:AAF27674.1; GSPDB:GN
C;Genetics:
A;Gene: T7P1.16
A;Map position: 1

  Query Match             12.9%;  Score 71.5;  DB 2;  Length 840;
  Best Local Similarity   19.3%;  Pred. No. 45;
  Matches   21;  Conservative   27;  Mismatches   50;  Indels   11;  Gaps    2;

Qy          4 PASEQETKVRPK---PKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              |     |||:|:    :|| ::| | | :|  :| :         : :  : |  |: :|
Db        192 PVVSASTKVKPRNIGSRLLSIIKDVDAARDAASMHD--------LSSCDIIDRAQEILVN 243

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
```

```
Db        244 CKELRLIDSYKIERMRPELSTKWVALLVMEKACLSKISFDDTSGTVKKS 292
```

RESULT 10
I45557
eyeless, long form - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 16-Aug-2004
C;Accession: I45557
R;Quiring, R.; Walldorf, U.; Kloter, U.; Gehring, W.J.
Science 265, 785-789, 1994
A;Title: Homology of the eyeless gene of Drosophila to the Small eye gene in mice and An
A;Reference number: A54584; MUID:94323757; PMID:7914031
A;Accession: I45557
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-838 <RES>
A;Cross-references: EMBL:X79493; NID:g641809; PIDN:CAA56038.1; PID:g641810
C;Genetics:
A;Gene: FlyBase:ey
A;Cross-references: FlyBase:FBgn0005558
A;Introns: 37/1; 92/2; 152/3; 371/1; 429/1; 521/1; 639/2
C;Superfamily: homeobox homology; paired box homology
C;Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulati
F;37-161/Domain: paired box homology <PBH>
F;412-468/Domain: homeobox homology <HOX>

  Query Match 12.8%; Score 71; DB 2; Length 838;
  Best Local Similarity 24.1%; Pred. No. 50;
  Matches 27; Conservative 17; Mismatches 40; Indels 28; Gaps 5;

```
Qy          1 SQIPASEQET-KVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQY------IMTKRLYDE 53
Db         87 SKILGRYYETGSIRP--------RAIGGSKPRVATAEVVSKISQYKRECPSIFAWEIRDR 138

Qy         54 KQQHIVKCSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTS 105
Db        139 LLQENV-CTNDNIPSVSSI------------NRVLRNLAAQKEQQSTGSGSS 177
```

RESULT 11
C69215
conserved hypothetical protein MTH863 - Methanobacterium thermoautotrophicum (strain Del
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: C69215
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: C69215
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-223 <MTH>
A;Cross-references: UNIPROT:O26951; GB:AE000862; GB:AE000666; NID:g2621943; PIDN:AAB8536
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH863
A;Start codon: TTG

  Query Match 12.7%; Score 70.5; DB 2; Length 223;
  Best Local Similarity 25.3%; Pred. No. 13;
  Matches 22; Conservative 21; Mismatches 27; Indels 17; Gaps 5;

```
Qy         28 QKDTYT-MKEVLHYLG-------QYIMTKRL-----YDEKQQHIVKCSNDKLGDLFGVKS 74
Db        102 EEDMFSHYRDFLHLRGADAFFTAEVVSVKKLVKRDRFGESELHVVKA---RAGDVMRAES 158

Qy         75 FSVKEHRKIYTMIYRNLVVVNQQESSD 101
Db        159 FRMALNRGIYAVI-ESLIAYTRAEFSD 184
```

RESULT 12
T15185
hypothetical protein C18E3.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15185
R;Connell, M.; Maggi, L.
submitted to the EMBL Data Library, April 1997
A;Description: The sequence of C. elegans cosmid C18E3.
A;Reference number: Z18304
A;Accession: T15185
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-525 <CON>
A;Cross-references: UNIPROT:O02101; EMBL:AF000265; NID:g1947147; PID:g1947150; PIDN:AAB5
A;Experimental source: strain Bristol N2; clone C18E3
C;Genetics:
A;Gene: CESP:C18E3.2
A;Map position: 1
A;Introns: 12/1; 70/3; 93/3; 141/3; 503/2

  Query Match 12.7%; Score 70.5; DB 2; Length 525;
  Best Local Similarity 24.5%; Pred. No. 33;
  Matches 24; Conservative 20; Mismatches 41; Indels 13; Gaps 4;

```
Qy         11 KVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVKCSNDKLGDLF 70
Db        303 KFKLHPRLAKVLGIA-----TETRPKIIEALWQYIKTHGLQDPQERDIINC-DTFLSQCF 356

Qy         71 GVKSFSVKE-HRKIYTMIYR------NLVVVNQQESSD 101
Db        357 GVNRMRFMEVPNKLHQLLQQTDPLEFNHIIQRPKEGQE 394
```

RESULT 13
S28062
homeotic protein globosa - garden snapdragon
C;Species: Antirrhinum majus (garden snapdragon)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: S28062
R;Troebner, W.; Ramirez, L.; Motte, P.; Hue, I.; Huijser, P.; Loennig, W.E.; Saedler, H.
EMBO J. 11, 4693-4704, 1992
A;Title: GLOBOSA: a homeotic gene which interacts with DEFICIENS in the control of Antir
A;Reference number: S28062; MUID:93099842; PMID:1361166
A;Accession: S28062
A;Molecule type: DNA
A;Residues: 1-215 <TRO>
A;Cross-references: UNIPROT:Q03378; EMBL:X68831; NID:g16023; PIDN:CAA48725.1; PID:g16024
C;Genetics:
A;Gene: glo
A;Introns: 63/2; 85/3; 106/2; 139/3; 149/3; 164/3
C;Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
C;Keywords: DNA binding; nucleus; transcription regulation
F;2-57/Domain: serum response factor DNA-binding domain homology <SRF>

  Query Match 12.6%; Score 70; DB 2; Length 215;
  Best Local Similarity 24.6%; Pred. No. 13;
  Matches 32; Conservative 28; Mismatches 38; Indels 32; Gaps 8;

```
Qy          2 QIPASEQETKVRPKPKLLKLL----------KSVGAQKD----TYTMKEVL-HYLGQYIM 46
Db         18 QVTYSKRRNGIMKKAKEISVLCDAHVSVIIFASSGKMHEFCSPSTTLVDMLDHY--HKLS 75

Qy         47 TKRLYDEKQQHI------VKCSNDKLG-DLFGVKSFSVKEHRKIYTMIYRNLVVVNQQES 99
Db         76 GKRLWDPKHEHLDNEINRVKKENDSMQIELRHLKG------EDITTLNYKELMVL--EDA 127

Qy        100 SDSGTSVSEN 109
Db        128 LENGTSALKN 137
```

RESULT 14
ZHBPG4
gene H protein - phage G4
C;Species: phage G4
C;Date: 30-Nov-1979 #sequence_revision 30-Nov-1979 #text_change 09-Jul-2004
C;Accession: A04255
R;Godson, G.N.; Barrell, B.G.; Staden, R.; Fiddes, J.C.
Nature 276, 236-247, 1978
A;Title: Nucleotide sequence of bacteriophage G4 DNA.
A;Reference number: A93200; MUID:79053264; PMID:714153
A;Accession: A04255
A;Molecule type: DNA
A;Residues: 1-337 <GOD>
A;Cross-references: UNIPROT:P03647; GB:J02454; GB:M10724; GB:M11404; GB:V00657; NID:g158
C;Comment: Gene H protein is the minor spike component of the viral shell.
C;Superfamily: phage phi-X174 gene H protein

Query Match 12.6%; Score 70; DB 1; Length 337;
Best Local Similarity 21.8%; Pred. No. 22;
Matches 26; Conservative 19; Mismatches 44; Indels 30; Gaps 3;

```
Qy          20 KLLKSVGAQKDTYTM-KEVLHYL----------------------------GQYIMTKRL 50
                  ||:::||  |       |:   ||                            |  :||
Db          94 KLMEAVGLSKSASDKGKDTKDYLAAAFPELNPWERAGAGASSPGMQDAGFQNQKELTKMQ 153

Qy          51 YDEKQQHIVKCSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
                |  |: | |  |:   :: |::| : :|: |        ::  ||:||     :: ||
Db         154 LD-NQKEIAKMQNETQKEIAGLQSITSRENTKDTVYAQNEMLAYNQKESMSRVGAILEN 211
```

RESULT 15
S70186
21K protein - Shigella flexneri
C;Species: Shigella flexneri
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 09-Jul-2004
C;Accession: S70186
R;Uchiya, K.; Tobe, T.; Komatsu, K.; Suzuki, T.; Watarai, M.; Fukuda, I.; Yoshikawa, M.;
Mol. Microbiol. 17, 241-250, 1995
A;Title: Identification of a novel virulence gene, virA, on the large plasmid of Shigell
A;Reference number: S70186; MUID:96079274; PMID:7494473
A;Accession: S70186
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-187 <UCH>
A;Cross-references: UNIPROT:Q52296; EMBL:D26468; NID:g992954; PIDN:BAA05481.1; PID:d1006
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1994

Query Match 12.5%; Score 69; DB 2; Length 187;
Best Local Similarity 21.6%; Pred. No. 14;
Matches 21; Conservative 17; Mismatches 31; Indels 28; Gaps 3;

```
Qy          23 KSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQ----------------HIVKCSNDKL 66
                  :|  ||:| :  ||:|          |:|||  |                 : :|:  :|
Db          40 RSARAQRDDWLKKEIL----------RVYDENHQVYAVRKVWHQLLREGIRVARCTVARL 89

Qy          67 GDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSG 103
                : |:    |   :|::| : |  |    : :   |
Db          90 MAVMGLA--GVLRGKKVHTTVSRKAVAAGDRVNRHQG 124
```

Search completed: January 27, 2005, 18:15:12
Job time : 20.8 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:51:46 ; Search time 84.6 Seconds
(without alignments)
741.322 Million cell updates/sec

Title: US-10-822-254-12
Perfect score: 554
Sequence: 1 SQIPASEQETKVRPKPKLLK.....NLVVVNQQESSDSGTSVSEN 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	511	92.2	166	2	Q8NDW2	Q8ndw2 homo sapien
2	511	92.2	195	2	Q96DS4	Q96ds4 homo sapien
3	511	92.2	243	2	Q8TE47	Q8te47 homo sapien
4	511	92.2	491	1	MDM2_HUMAN	Q00987 homo sapien
5	511	92.2	491	2	AAP35922	Aap35922 homo sapi
6	511	92.2	491	2	AAH67077	Aah67077 homo sapi
7	499	90.1	487	1	MDM2_CANFA	P56950 canis famil
8	499	90.1	487	2	Q9GMZ6	Q9gmz6 canis famil
9	499	90.1	491	1	MDM2_HORSE	P56951 equus cabal
10	496	89.5	491	2	Q7YRZ8	Q7yrz8 felis silve
11	461	83.2	436	2	Q8WYJ2	Q8wyj2 homo sapien
12	451.5	81.5	489	1	MDM2_MOUSE	P23804 mus musculu
13	451.5	81.5	489	2	Q91XK7	Q91xk7 m mus muscu
14	434	78.3	118	2	Q8WYJ3	Q8wyj3 homo sapien
15	433.5	78.2	466	1	MDM2_MESAU	Q60524 mesocricetu
16	387	69.9	325	2	Q9PVL2	Q9pvl2 gallus gall
17	365	65.9	173	2	Q8TE46	Q8te46 homo sapien
18	346	62.5	473	1	MDM2_XENLA	P56273 xenopus lae
19	346	62.5	473	2	Q6GMB5	Q6gmb5 xenopus lae
20	345	62.3	482	2	Q6P3Q9	Q6p3q9 xenopus tro
21	345	62.3	482	2	AAH63898	Aah63898 xenopus t
22	311	56.1	105	2	Q8NDW0	Q8ndw0 homo sapien
23	297	53.6	426	2	Q9GK41	Q9gk41 canis famil
24	287.5	51.9	445	1	MDM2_BRARE	O42354 brachydanio
25	287.5	51.9	445	2	AAM00198	Aam00198 brachydan
26	281	50.7	491	2	Q7ZUW7	Q7zuw7 brachydanio
27	278.5	50.3	489	1	MDM4_MOUSE	O35618 mus musculu
28	275.5	49.7	489	2	Q9CYG1	Q9cyg1 m mus muscu
29	270	48.7	475	2	Q7ZYI3	Q7zyi3 xenopus lae
30	269	48.6	490	2	Q99L86	Q99l86 mus musculu
31	268.5	48.5	446	2	Q8WYJ1	Q8wyj1 homo sapien
32	258.5	46.7	134	2	Q6PHL8	Q6phl8 xenopus lae
33	258.5	46.7	134	2	AAH56503	Aah56503 xenopus l
34	252	45.5	153	2	Q6MZR7	Q6mzr7 homo sapien
35	252	45.5	153	2	CAE45961	Cae45961 homo sapi
36	252	45.5	490	2	AAH67299	Aah67299 homo sapi
37	250	45.1	490	1	MDM4_HUMAN	O15151 homo sapien
38	204	36.8	69	2	Q86WA4	Q86wa4 homo sapien
39	197	35.6	66	2	Q96DS3	Q96ds3 homo sapien
40	194	35.0	70	2	Q86WA3	Q86wa3 homo sapien
41	181	32.7	95	2	Q96DS1	Q96ds1 homo sapien
42	168	30.3	159	2	Q96DS0	Q96ds0 homo sapien
43	165	29.8	70	2	Q8NDW1	Q8ndw1 homo sapien
44	164	29.6	60	2	Q96DS5	Q96ds5 homo sapien
45	164	29.6	130	2	Q9H4C3	Q9h4c3 homo sapien

ALIGNMENTS

RESULT 1
Q8NDW2
ID Q8NDW2 PRELIMINARY; PRT; 166 AA.
AC Q8NDW2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE P53-binding protein.
GN Name=MDM2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bartel F., Pinkert D., Kappler M., Bache M., Schmidt H., Taubert H.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ491698; CAD36959.1; -.
DR HSSP; Q9UMT8; 1YCR.
DR GO; GO:0005634; C:nucleus; IEA.
DR InterPro; IPR010984; MDM2.
DR InterPro; IPR003121; SWIB_MDM2.
DR Pfam; PF02201; SWIB; 1.
SQ SEQUENCE 166 AA; 18900 MW; FA6B5BA18E85040D CRC64;

Query Match 92.2%; Score 511; DB 2; Length 166;
Best Local Similarity 94.5%; Pred. No. 4.6e-43;
Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              ||||||||||  ||||| ||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125
```

RESULT 2
Q96DS4
ID Q96DS4 PRELIMINARY; PRT; 195 AA.
AC Q96DS4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MDM2 variant FB26.
GN Name=MDM2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Rhabdomyosarcoma tumor;

```
RA   Bartel F., Taylor A.C., Taubert H., Harris L.C.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF385323; AAL13243.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB_MDM2.
DR   Pfam; PF02201; SWIB; 1.
SQ   SEQUENCE   195 AA;  22161 MW;  4987AE567DB12D5D CRC64;

  Query Match             92.2%;  Score 511;  DB 2;  Length 195;
  Best Local Similarity   94.5%;  Pred. No. 5.5e-43;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              |||||||||| ||||| ||||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 3
Q8TE47
ID   Q8TE47      PRELIMINARY;      PRT;   243 AA.
AC   Q8TE47;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   MDM2 isoform KB9 protein.
GN   Name=MDM2 isoform KB9;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymphocytes;
RA   Bartel F., Pinkert D., Kappler M., Bache M., Schmidt H., Taubert H.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ430612; CAD23251.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR   GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   GO; GO:0016567; P:protein ubiquitination; IEA.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB_MDM2.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
SQ   SEQUENCE   243 AA;  27317 MW;  9EB5D0142CF185A2 CRC64;

  Query Match             92.2%;  Score 511;  DB 2;  Length 243;
  Best Local Similarity   94.5%;  Pred. No. 7e-43;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              |||||||||| ||||| ||||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 4
MDM2_HUMAN
ID   MDM2_HUMAN     STANDARD;      PRT;   491 AA.
AC   Q00987; Q13226; Q13297; Q13298; Q13299; Q13300; Q13301; Q9UGI3;
AC   Q9UMT8;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein
DE   Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Hdm2).
GN   Name=MDM2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM MDM2).
RX   MEDLINE=92310576; PubMed=1614537;
RA   Oliner J.D., Kinzler K.W., Meltzer P.S., George D.L., Vogelstein B.;
RT   "Amplification of a gene encoding a p53-associated protein in human
RT   sarcomas.";
RL   Nature 358:80-83(1992).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS MDM2-A; -B; -C; -D AND -E).
RC   TISSUE=Ovarian carcinoma;
RX   MEDLINE=96313107; PubMed=8705862;
RA   Sigalas I., Calvert A.H., Anderson J.J., Neal D.E., Lunec J.;
RT   "Alternatively spliced mdm2 transcripts with loss of p53 binding
RT   domain sequences: transforming ability and frequent detection in human
RT   cancer.";
RL   Nat. Med. 2:912-917(1996).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM MDM2-ALPHA).
RX   MEDLINE=20065171; PubMed=10597303;
RA   Veldhoen N., Metcalfe S., Milner J.;
RT   "A novel exon within the mdm2 gene modulates translation initiation in
RT   vitro and disrupts the p53-binding domain of mdm2 protein.";
RL   Oncogene 18:7026-7033(1999).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM MDM2).
RA   Rieder M.J., Livingston R.J., Braun A.C., Montoya M.A., Chung M.-W.,
RA   Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA   Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RT   "NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department
RT   of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM MDM2).
RC   TISSUE=Muscle;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [6]
RP   SEQUENCE OF 6-491 FROM N.A. (ISOFORM MDM2-A1).
RA   Liang H., Atkins H., Abdel-Fattah R., Suaeyun R., Lunec J.;
RT   "Genomic organisation of the human MDM2 oncogene and relationship to
RT   its alternatively spliced mRNA's.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
RN   [7]
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RP   SEQUENCE OF 1-24 FROM N.A.
RX   MEDLINE=95380270; PubMed=7651818;
RA   Zauberman A., Flusberg D., Haupt Y., Barak Y., Oren M.;
RT   "A functional p53-responsive intronic promoter is contained within the
RT   human mdm2 gene.";
RL   Nucleic Acids Res. 23:2584-2592(1995).
RN   [8]
RP   SEQUENCE OF 1-9 FROM N.A.
RX   MEDLINE=97413643; PubMed=9270029;
RA   Landers J.E., Cassel S.L., George D.L.;
RT   "Translational enhancement of mdm2 oncogene expression in human tumor
RT   cells containing a stabilized wild-type p53 protein.";
RL   Cancer Res. 57:3562-3568(1997).
RN   [9]
RP   SEQUENCE OF 301-481 FROM N.A.
RX   MEDLINE=20542019; PubMed=11087894;
RA   Taubert H., Kappler M., Meye A., Bartel F., Schlott T.,
RA   Lautenschlaeger C., Bache M., Schmidt H., Wuerl P.;
RT   "A MboII polymorphism in exon 11 of the human MDM2 gene occuring in
RT   normal blood donors and in soft tissue sarcoma patients: an indication
RT   for an increased cancer susceptibility?";
RL   Mutat. Res. 456:39-44(2000).
RN   [10]
RP   MUTAGENESIS OF CYS-464.
RX   MEDLINE=98111004; PubMed=9450543;
RA   Honda R., Tanaka H., Yasuda H.;
RT   "Oncoprotein MDM2 is a ubiquitin ligase E3 for tumor suppressor p53.";
RL   FEBS Lett. 420:25-27(1997).
RN   [11]
RP   MUTAGENESIS OF CYS-449.
RX   MEDLINE=20190101; PubMed=10723139;
RA   Honda R., Yasuda H.;
RT   "Activity of MDM2, a ubiquitin ligase, toward p53 or itself is
RT   dependent on the RING finger domain of the ligase.";
RL   Oncogene 19:1473-1476(2000).
RN   [12]
RP   MUTAGENESIS.
RX   MEDLINE=20187618; PubMed=10722742;
RA   Fang S., Jensen J.P., Ludwig R.L., Vousden K.H., Weissman A.M.;
RT   "Mdm2 is a RING finger-dependent ubiquitin protein ligase for itself
RT   and p53.";
RL   J. Biol. Chem. 275:8945-8951(2000).
RN   [13]
RP   MUTAGENESIS OF CYS-441 AND CYS-478.
RX   MEDLINE=20076498; PubMed=10608892;
RA   Sharp D.A., Kratowicz S.A., Sank M.J., George D.L.;
RT   "Stabilization of the MDM2 oncoprotein by interaction with the
RT   structurally related MDMX protein.";
RL   J. Biol. Chem. 274:38189-38196(1999).
RN   [14]
RP   NUCLEOLAR LOCALIZATION SIGNAL.
RX   MEDLINE=20173879; PubMed=10707090;
RA   Lohrum M.A.E., Ashcroft M., Kubbutat M.H.G., Vousden K.H.;
RT   "Identification of a cryptic nucleolar-localization signal in MDM2.";
RL   Nat. Cell Biol. 2:179-181(2000).
RN   [15]
RP   PHOSPHORYLATION BY ATM.
RX   MEDLINE=20079591; PubMed=10611322;
RA   Khosravi R., Maya R., Gottlieb T., Oren M., Shiloh Y., Shkedy D.;
RT   "Rapid ATM-dependent phosphorylation of MDM2 precedes p53 accumulation
RT   in response to DNA damage.";
RL   Proc. Natl. Acad. Sci. U.S.A. 96:14973-14977(1999).
RN   [16]
RP   X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 25-109 IN COMPLEX WITH P53.
RX   MEDLINE=97081050; PubMed=8875929;
RA   Kussie P.H., Gorina S., Marechal V., Elenbaas B., Moreau J.,
RA   Levine A.J., Pavletich N.P.;
RT   "Structure of the MDM2 oncoprotein bound to the p53 tumor suppressor
RT   transactivation domain.";
RL   Science 274:948-953(1996).
CC   -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC       apoptosis by binding its transcriptional activation domain.
CC       Functions as a ubiquitin ligase E3, in the presence of E1 and E2,
CC       toward p53 and itself. Permits the nuclear export of p53 and
CC       targets it for proteasome-mediated proteolysis.
CC   -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity.
CC   -!- SUBUNIT: Binds p53, p73, ARF(P14), ribosomal protein L5 and
CC       specifically to RNA. Can interact also with retinoblastoma protein
CC       (RB), E1A-associated protein EP300 and the E2F1 transcription
CC       factor.
CC   -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed
CC       predominantly in the nucleoplasm. Interaction with ARF(P14)
CC       results in the localization of both proteins to the nucleolus. The
CC       nucleolar localization signals in both ARF(P14) and MDM2 may be
CC       necessary to allow efficient nucleolar localization of both
CC       proteins.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=8;
CC       Name=Mdm2;
CC         IsoId=Q00987-1; Sequence=Displayed;
CC       Name=Mdm2-A;
CC         IsoId=Q00987-2; Sequence=VSP_003208;
CC       Name=Mdm2-A1;
CC         IsoId=Q00987-3; Sequence=VSP_003208, VSP_003214;
CC       Name=Mdm2-B;
CC         IsoId=Q00987-4; Sequence=VSP_003209;
CC       Name=Mdm2-C;
CC         IsoId=Q00987-5; Sequence=VSP_003211;
CC       Name=Mdm2-D;
CC         IsoId=Q00987-6; Sequence=VSP_003210;
CC       Name=Mdm2-E;
CC         IsoId=Q00987-7; Sequence=VSP_003212, VSP_003213;
CC       Name=Mdm2-alpha;
CC         IsoId=Q00987-8; Sequence=VSP_003207;
CC   -!- TISSUE SPECIFICITY: Ubiquitous. Isoforms MDM2-A, -B, -C, -D and -E
CC       are observed in a range of human cancers but absent in normal
CC       tissues.
CC   -!- INDUCTION: By DNA damage.
CC   -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its
CC       G1 arrest and apoptosis functions. It also binds p73 and E2F1.
CC       Region II contains most of a central acidic region required for
CC       interaction with ribosomal protein L5 and a putative C4-type zinc
CC       finger. The RING finger domain which coordinates two molecules of
CC       zinc interacts specifically with RNA whether or not zinc is
CC       present and mediates the hetero-oligomerization with MDM4. It is
CC       also essential for its ubiquitin ligase E3 activity toward p53 and
CC       itself.
CC   -!- PTM: Phosphorylated in response to ionizing radiation in an ATM-
CC       dependent manner.
CC   -!- DISEASE: Seems to be amplified in certain tumors (including soft
CC       tissue sarcomas, osteosarcomas and gliomas). A higher frequency of
CC       splice variants lacking p53 binding domain sequences was found in
CC       late-stage and high-grade ovarian and bladder carcinomas. Four of
CC       the splice variants show loss of p53 binding.
CC   -!- MISCELLANEOUS: MDM2 RING finger mutations that failed to

  Query Match             92.2%;  Score 511;  DB 1;  Length 491;
  Best Local Similarity   94.5%;  Pred. No. 1.5e-42;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              ||||||||||  ||||| ||||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 5
AAP35922
ID   AAP35922    PRELIMINARY;      PRT;   491 AA.
AC   AAP35922;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
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DE   Mdm2, transformed 3T3 cell double minute 2, p53 binding protein
DE   (Mouse).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA   Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA   Phelan M., Farmer A.;
RT   "Cloning of human full-length CDSs in BD Creator(TM) System Donor
RT   vector.";
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BT007258; AAP35922.1; -.
SQ   SEQUENCE   491 AA;  55232 MW;  F37CE163876BC983 CRC64;

  Query Match             92.2%;  Score 511;  DB 2;  Length 491;
  Best Local Similarity   94.5%;  Pred. No. 1.5e-42;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 6
AAH67077
ID   AAH67077    PRELIMINARY;      PRT;   491 AA.
AC   AAH67077;
DT   14-APR-2004 (TrEMBLrel. 27, Created)
DT   14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT   14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle;
RA   Strausberg R.;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC067077; AAH67077.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   491 AA;  55232 MW;  F37CE163876BC983 CRC64;

  Query Match             92.2%;  Score 511;  DB 2;  Length 491;
  Best Local Similarity   94.5%;  Pred. No. 1.5e-42;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 7
MDM2_CANFA
ID   MDM2_CANFA     STANDARD;      PRT;   487 AA.
AC   P56950; Q95KN5;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein
DE   Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Cdm2).
GN   Name=MDM2;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE OF 1-484 FROM N.A.
RX   MEDLINE=20218866; PubMed=10754200;
RA   Nasir L., Burr P.D., McFarlane S.T., Gault E., Thompson H.,
RA   Argyle D.J.;
RT   "Cloning, sequence analysis and expression of the cDNAs encoding the
RT   canine and equine homologues of the mouse double minute 2 (mdm2)
RT   proto-oncogene.";
RL   Cancer Lett. 152:9-13(2000).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS MDM2 AND MDM2-ALPHA).
RX   MEDLINE=20065171; PubMed=10597303;
RA   Veldhoen N., Metcalfe S., Milner J.;
RT   "A novel exon within the mdm2 gene modulates translation initiation in
RT   vitro and disrupts the p53-binding domain of mdm2 protein.";
RL   Oncogene 18:7026-7033(1999).
CC   -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC       apoptosis by binding its transcriptional activation domain.
CC       Functions as a ubiquitin ligase E3, in the presence of E1 and E2,
CC       toward p53 and itself. Permits the nuclear export of p53 and
CC       targets it for proteasome-mediated proteolysis (By similarity).
CC   -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity (By
CC       similarity).
CC   -!- SUBUNIT: Binds p53, p73, ARF(P14), ribosomal protein L5 and
CC       specifically to RNA. Can interact also with retinoblastoma protein
CC       (RB), E1A-associated protein EP300 and the E2F1 transcription
CC       factor (By similarity).
CC   -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed
CC       predominantly in the nucleoplasm (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Mdm2;
CC         IsoId=P56950-1; Sequence=Displayed;
CC       Name=Mdm2-alpha;
CC         IsoId=P56950-2; Sequence=VSP_003206;
CC   -!- TISSUE SPECIFICITY: Isoform Mdm2-alpha is present in lymphoid and
CC       testicular tissues.
CC   -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its
CC       G1 arrest and apoptosis functions. It also binds p73 and E2F1.
CC       Region II contains most of a central acidic region required for
CC       interaction with ribosomal protein L5 and a putative C4-type zinc
CC       finger. The RING finger domain which coordinates two molecules of
CC       zinc interacts specifically with RNA whether or not zinc is
CC       present and mediates the hetero-oligomerization with MDM4. It is
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CC       also essential for its ubiquitin ligase E3 activity toward p53 and
CC       itself (By similarity).
CC   -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.
CC   -!- SIMILARITY: Contains 1 RanBP2-type zinc finger.
CC   -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC   -!- SIMILARITY: Contains 1 SWIB domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF100705; AAF67833.1; -.
DR   EMBL; AF322416; AAG42840.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Alternative splicing; Ligase; Metal-binding; Nuclear protein;
KW   Ubl conjugation pathway; Zinc; Zinc-finger.
FT   DOMAIN       27    107       SWIB.
FT   DOMAIN      179    185       Nuclear localization signal (Potential).
FT   DOMAIN      190    202       Nuclear export signal.
FT   DOMAIN      210    304       ARF-binding.
FT   DOMAIN      210    215       Poly-Ser.
FT   DOMAIN      242    331       Region II.
FT   DOMAIN      243    301       Asp/Glu-rich (acidic).
FT   ZN_FING     299    328       RanBP2-type.
FT   ZN_FING     434    475       RING-type.
FT   DOMAIN      462    469       Nucleolar localization signal
FT                                (Potential).
FT   VARSPLIC      1     61       Missing (in isoform Mdm2-alpha).
FT                                /FTId=VSP_003206.
FT   CONFLICT     11     11       G -> D (in Ref. 2).
FT   CONFLICT    238    239       QD -> HH (in Ref. 2).
SQ   SEQUENCE   487 AA;  54696 MW;  60CDB470A32A8E69 CRC64;

  Query Match             90.1%;  Score 499;  DB 1;  Length 487;
  Best Local Similarity   91.7%;  Pred. No. 2.4e-41;
  Matches  100;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              |||||||||| ||||| ||||||||||||||||||||: ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVIFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||||||||||| | ||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQHEPSDSGTSVSEN 125


RESULT 8
Q9GMZ6
ID   Q9GMZ6       PRELIMINARY;      PRT;   487 AA.
AC   Q9GMZ6;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   MDM2.
GN   Name=mdm2;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Setoguchi A., Tsujimoto H.;
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB031276; BAB11975.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   GO; GO:0005730; C:nucleolus; ISS.
DR   GO; GO:0005654; C:nucleoplasm; ISS.
DR   GO; GO:0017163; F:negative regulator of basal transcription a. . .; ISS.
DR   GO; GO:0005515; F:protein binding; ISS.
DR   GO; GO:0000122; P:negative regulation of transcription from P. . .; ISS.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB_MDM2.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
SQ   SEQUENCE   487 AA;  54724 MW;  34FC5CC6A18D7744 CRC64;

  Query Match             90.1%;  Score 499;  DB 2;  Length 487;
  Best Local Similarity   91.7%;  Pred. No. 2.4e-41;
  Matches  100;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              |||||||||| ||||| ||||||||||||||||||||: ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVIFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||||||||||| | ||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQHEPSDSGTSVSEN 125


RESULT 9
MDM2_HORSE
ID   MDM2_HORSE     STANDARD;      PRT;   491 AA.
AC   P56951;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein
DE   Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Edm2).
GN   Name=MDM2;
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20218866; PubMed=10754200;
RA   Nasir L., Burr P.D., McFarlane S.T., Gault E., Thompson H.,
RA   Argyle D.J.;
RT   "Cloning, sequence analysis and expression of the cDNAs encoding the
RT   canine and equine homologues of the mouse double minute 2 (mdm2)
RT   proto-oncogene.";
RL   Cancer Lett. 152:9-13(2000).
CC   -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC       apoptosis by binding its transcriptional activation domain.
CC       Functions as a ubiquitin ligase E3, in the presence of E1 and E2,
CC       toward p53 and itself. Permits the nuclear export of p53 and
CC       targets it for proteasome-mediated proteolysis (By similarity).
CC   -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity (By
CC       similarity).
CC   -!- SUBUNIT: Binds p53, p73, ARF(P14), ribosomal protein L5 and
CC       specifically to RNA. Can interact also with retinoblastoma protein
CC       (RB), E1A-associated protein EP300 and the E2F1 transcription
CC       factor (By similarity).
CC   -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed
```

```
CC       predominantly in the nucleoplasm (By similarity).
CC   -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its
CC       G1 arrest and apoptosis functions. It also binds p73 and E2F1.
CC       Region II contains most of a central acidic region required for
CC       interaction with ribosomal protein L5 and a putative C4-type zinc
CC       finger. The RING finger domain which coordinates two molecules of
CC       zinc interacts specifically with RNA whether or not zinc is
CC       present and mediates the hetero-oligomerization with MDM4. It is
CC       also essential for its ubiquitin ligase E3 activity toward p53 and
CC       itself (By similarity).
CC   -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.
CC   -!- SIMILARITY: Contains 1 RanBP2-type zinc finger.
CC   -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC   -!- SIMILARITY: Contains 1 SWIB domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF121140; AAF28866.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Ligase; Metal-binding; Nuclear protein; Ubl conjugation pathway; Zinc;
KW   Zinc-finger.
FT   DOMAIN       27    107       SWIB.
FT   DOMAIN      179    185       Nuclear localization signal (Potential).
FT   DOMAIN      190    202       Nuclear export signal.
FT   DOMAIN      210    304       ARF-binding.
FT   DOMAIN      210    215       Poly-Ser.
FT   DOMAIN      242    331       Region II.
FT   DOMAIN      243    301       Asp/Glu-rich (acidic).
FT   ZN_FING     299    328       RanBP2-type.
FT   ZN_FING     438    479       RING-type.
FT   DOMAIN      466    473       Nucleolar localization signal
FT                                (Potential).
SQ   SEQUENCE   491 AA;  55279 MW;  641E033D5C1DEC39 CRC64;

  Query Match             90.1%;  Score 499;  DB 1;  Length 491;
  Best Local Similarity   91.7%;  Pred. No. 2.4e-41;
  Matches  100;  Conservative    2;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              |||||||||| ||||| |||||||||||||||||||: ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVIFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||||||||:||| ||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVSQQEPSDSGTSVSEN 125


RESULT 10
Q7YRZ8
ID   Q7YRZ8      PRELIMINARY;      PRT;   491 AA.
AC   Q7YRZ8;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Double minute 2 protein MDM2.
GN   Name=mdm2;
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Miki R., Okuda M., Ma Z., Inokuma H., Onishi T.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB099709; BAC78209.1; -.
DR   GO; GO:0005730; C:nucleolus; ISS.
DR   GO; GO:0005654; C:nucleoplasm; ISS.
DR   GO; GO:0017163; F:negative regulator of basal transcription a. . .; ISS.
DR   GO; GO:0005515; F:protein binding; ISS.
DR   GO; GO:0000122; P:negative regulation of transcription from P. . .; ISS.
DR   InterPro; IPR003121; SWIB_MDM2.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
SQ   SEQUENCE   491 AA;  55433 MW;  D93E25D638E88934 CRC64;

  Query Match             89.5%;  Score 496;  DB 2;  Length 491;
  Best Local Similarity   90.8%;  Pred. No. 4.9e-41;
  Matches   99;  Conservative    2;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              ||:||||||| ||||| |||||||||||||||||||: ||||||||||||||||||||
Db         17 SQMPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVIFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||||||||||| | ||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQHEPSDSGTSVSEN 125


RESULT 11
Q8WYJ2
ID   Q8WYJ2      PRELIMINARY;      PRT;   436 AA.
AC   Q8WYJ2;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   MDM2 protein.
GN   Name=MDM2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21248713; PubMed=11351297;
RA   Tamborini E., Della Torre G., Lavarino C., Azzarelli A.,
RA   Carpinelli P., Pierotti M.A., Pilotti S.;
RT   "Analysis of the molecular species generated by MDM2 gene
RT   amplification in liposarcomas.";
RL   Int. J. Cancer 92:790-796(2001).
DR   EMBL; AF092844; AAL40179.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   GO; GO:0005730; C:nucleolus; ISS.
DR   GO; GO:0005654; C:nucleoplasm; ISS.
DR   GO; GO:0017163; F:negative regulator of basal transcription a. . .; ISS.
DR   GO; GO:0005515; F:protein binding; ISS.
DR   GO; GO:0000122; P:negative regulation of transcription from P. . .; ISS.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB_MDM2.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
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DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
SQ   SEQUENCE   436 AA;  49248 MW;  3C8F55E98BC4203A CRC64;

  Query Match           83.2%;  Score 461;  DB 2;  Length 436;
  Best Local Similarity   88.6%;  Pred. No. 1.3e-37;
  Matches   93;  Conservative    1;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              ||||||||| ||||| ||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTS 105
              |||| ||||||| |||||||||||||||||||||||| :    |
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQEENSDELS 121


RESULT 12
MDM2_MOUSE
ID   MDM2_MOUSE     STANDARD;      PRT;   489 AA.
AC   P23804; Q61040; Q64330;
DT   01-NOV-1991 (Rel. 20, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein
DE   Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein).
GN   Name=Mdm2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM MDM2-P90).
RX   MEDLINE=91224107; PubMed=2026149;
RA   Fakharzadeh S.S., Trusko S.P., George D.L.;
RT   "Tumorigenic potential associated with enhanced expression of a gene
RT   that is amplified in a mouse tumor cell line.";
RL   EMBO J. 10:1565-1569(1991).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM MDM2-P90).
RC   STRAIN=129/Sv;
RX   MEDLINE=97074674; PubMed=8917101;
RA   Jones S.N., Ansari-Lari M.A., Hancock A.R., Jones W.J., Gibbs R.A.,
RA   Donehower L.A., Bradley A.;
RT   "Genomic organization of the mouse double minute 2 gene.";
RL   Gene 175:209-213(1996).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM MDM2-P90).
RC   STRAIN=129/Sv;
RX   MEDLINE=96299630; PubMed=8660994;
RA   de Oca Luna R.M., Tabor A.D., Eberspaecher H., Hulboy D.L.,
RA   Worth L.L., Colman M.S., Finlay C.A., Lozano G.;
RT   "The organization and expression of the mdm2 gene.";
RL   Genomics 33:352-357(1996).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORMS MDM2-P90 AND MDM2-P76).
RX   MEDLINE=99175199; PubMed=10075719;
RA   Saucedo L.J., Myers C.D., Perry M.E.;
RT   "Multiple murine double minute gene 2 (MDM2) proteins are induced by
RT   ultraviolet light.";
RL   J. Biol. Chem. 274:8161-8168(1999).
RN   [5]
RP   NUCLEOLAR LOCALIZATION SIGNAL.
RX   MEDLINE=20180080; PubMed=10713175;
RA   Weber J.D., Kuo M.-L., Bothner B., DiGiammarino E.L., Kriwacki R.W.,
RA   Roussel M.F., Sherr C.J.;
RT   "Cooperative signals governing ARF-mdm2 interaction and nucleolar
RT   localization of the complex.";
RL   Mol. Cell. Biol. 20:2517-2528(2000).
RN   [6]
RP   PHOSPHORYLATION BY ATM.
RX   MEDLINE=20079591; PubMed=10611322;
RA   Khosravi R., Maya R., Gottlieb T., Oren M., Shiloh Y., Shkedy D.;
RT   "Rapid ATM-dependent phosphorylation of MDM2 precedes p53 accumulation
RT   in response to DNA damage.";
RL   Proc. Natl. Acad. Sci. U.S.A. 96:14973-14977(1999).
CC   -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC       apoptosis by binding its transcriptional activation domain.
CC       Functions as a ubiquitin ligase E3, in the presence of E1 and E2,
CC       toward p53 and itself. Permits the nuclear export of p53 and
CC       targets it for proteasome-mediated proteolysis.
CC   -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity.
CC   -!- SUBUNIT: Binds p53, p73, ARF(P14), ribosomal protein L5 and
CC       specifically to RNA. Can interact also with retinoblastoma protein
CC       (RB), E1A-associated protein EP300 and the E2F1 transcription
CC       factor.
CC   -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed
CC       predominantly in the nucleoplasm. Interaction with ARF(P14)
CC       results in the localization of both proteins to the nucleolus. The
CC       nucleolar localization signals in both ARF(P14) and MDM2 may be
CC       necessary to allow efficient nucleolar localization of both
CC       proteins.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Mdm2-p90;
CC         IsoId=P23804-1; Sequence=Displayed;
CC         Note=Isoform Mdm2-p76 can also be produced by alternative
CC         initiation at Met-50 of isoform Mdm2-p90, but is produced more
CC         efficiently by alternative splicing;
CC       Name=Mdm2-p76;
CC         IsoId=P23804-2; Sequence=VSP_003215;
CC         Note=Does not bind to p53;
CC       Event=Alternative initiation;
CC         Comment=2 isoforms, Mdm2-p90 (shown here) and Mdm2-p76, are
CC         produced by alternative initiation at Met-1 and Met-50. Isoform
CC         Mdm2-p76 is produced more efficiently by alternative splicing;
CC   -!- TISSUE SPECIFICITY: Ubiquitously expressed at low-level throughout
CC       embryo development and in adult tissues. MDM2-p90 is much more
CC       abundant than MDM2-p76 in testis, brain, heart, and kidney, but in
CC       the thymus, spleen, and intestine, the levels of the MDM2 proteins
CC       are roughly equivalent.
CC   -!- INDUCTION: By UV light.
CC   -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its
CC       G1 arrest and apoptosis functions. It also binds p73 and E2F1.
CC       Region II contains most of a central acidic region required for
CC       interaction with ribosomal protein L5 and a putative C4-type zinc
CC       finger. The RING finger domain which coordinates two molecules of
CC       zinc interacts specifically with RNA whether or not zinc is
CC       present and mediates the hetero-oligomerization with MDM4. It is
CC       also essential for its ubiquitin ligase E3 activity toward p53 and
CC       itself.
CC   -!- PTM: Phosphorylated in response to ionizing radiation in an ATM-
CC       dependent manner.
CC   -!- DISEASE: The gene for this protein is amplified in a mouse tumor
CC       cell line.
CC   -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.
CC   -!- SIMILARITY: Contains 1 RanBP2-type zinc finger.
CC   -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC   -!- SIMILARITY: Contains 1 SWIB domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X58876; CAA41684.1; -.
DR   EMBL; U40145; AAA91167.1; -.
DR   EMBL; U47944; AAB09030.1; -.
DR   EMBL; U47935; AAB09030.1; JOINED.
DR   EMBL; U47936; AAB09030.1; JOINED.
DR   EMBL; U47937; AAB09030.1; JOINED.
DR   EMBL; U47938; AAB09030.1; JOINED.
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DR   EMBL; U47939; AAB09030.1; JOINED.
DR   EMBL; U47940; AAB09030.1; JOINED.
DR   EMBL; U47941; AAB09030.1; JOINED.
DR   EMBL; U47942; AAB09030.1; JOINED.
DR   EMBL; U47943; AAB09030.1; JOINED.
DR   EMBL; U47934; AAB09031.1; -.
DR   PIR; S15349; S15349.
DR   HSSP; Q9UMT8; 1YCR.
DR   MGD; MGI:96952; Mdm2.
DR   GO; GO:0005634; C:nucleus; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0004842; F:ubiquitin-protein ligase activity; IDA.
DR   GO; GO:0030163; P:protein catabolism; IDA.
DR   GO; GO:0016567; P:protein ubiquitination; IDA.
DR   GO; GO:0007089; P:traversing start control point of mitotic c. . .; IDA.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Alternative initiation; Alternative splicing; Ligase; Metal-binding;
KW   Nuclear protein; Phosphorylation; Proto-oncogene;
KW   Ubl conjugation pathway; Zinc; Zinc-finger.
FT   CHAIN         1    489       Ubiquitin-protein ligase E3 Mdm2, isoform
FT                                Mdm2-p90.
FT   CHAIN        50    489       ubiquitin-protein ligase E3 Mdm2, isoform
FT                                Mdm2-p76.
FT   INIT_MET      50     50       For isoform Mdm2-p76.
FT   DOMAIN        27    107       SWIB.
FT   DOMAIN       176    182       Nuclear localization signal (Potential).
FT   DOMAIN       183    195       Nuclear export signal.
FT   DOMAIN       203    213       Poly-Ser.
FT   DOMAIN       208    302       ARF-binding.
FT   DOMAIN       240    329       Region II.
FT   DOMAIN       221    299       Asp/Glu-rich (acidic).
FT   ZN_FING      297    326       RanBP2-type.
FT   ZN_FING      436    477       RING-type.
FT   DOMAIN       464    471       Nucleolar localization signal
FT                                (Potential).
FT   VARSPLIC       1     49       Missing (in isoform Mdm2-p76).
FT                                /FTId=VSP_003215.
FT   CONFLICT     203    203       S -> T (in Ref. 1).
FT   CONFLICT     419    419       D -> H (in Ref. 1).
FT   CONFLICT     486    486       S -> T (in Ref. 3).
SQ   SEQUENCE   489 AA;  54543 MW;  4ABF489E92038DF4 CRC64;

  Query Match             81.5%;  Score 451.5;  DB 1;  Length 489;
  Best Local Similarity   82.6%;  Pred. No. 1.4e-36;
  Matches   90;  Conservative    7;  Mismatches    9;  Indels    3;  Gaps    1;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              ||||||||||| ||||| |||||||||||| |||||||:: |:|||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQNDTYTMKEIIFYIGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| |||:||| |||||||||||| ||||||| |:||   |||||:||:
Db         77 CSNDLLGDVFGVPSFSVKEHRKIYAMIYRNLVAVSQQ---DSGTSLSES 122


RESULT 13
Q91XK7
ID   Q91XK7      PRELIMINARY;      PRT;   489 AA.
AC   Q91XK7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Mus musculus adult male lung cDNA, RIKEN full-length enriched library,
DE   clone:1200011P22 product:transformed mouse 3T3 cell double minute 2,
DE   full insert sequence (Transformed mouse 3T3 cell double minute 2) (Mus
DE   musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length
DE   enriched library, clone:E430022B10 product:transformed mouse 3T3 cell
DE   double minute 2, full insert sequence).
GN   Name=Mdm2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;
RX   MEDLINE=99279253; PubMed=10349636;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;
RX   MEDLINE=21085660; PubMed=11217851;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;
RX   MEDLINE=20499374; PubMed=11042159;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;
RX   MEDLINE=20530913; PubMed=11076861;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Lung;
RA   Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA   Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA   Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA   Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA   Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA   Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA   Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA   Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA   Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA   Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Mouse;
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RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [8]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Mouse;
RA   Strausberg R.;
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
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RC   STRAIN=NOD; TISSUE=Thymus;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK004719; BAB23502.1; -.
DR   EMBL; BC050902; AAH50902.1; -.
DR   EMBL; AK088638; BAC40470.1; -.
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DR   GO; GO:0005730; C:nucleolus; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0004842; F:ubiquitin-protein ligase activity; IDA.
DR   GO; GO:0030163; P:protein catabolism; IDA.
DR   GO; GO:0016567; P:protein ubiquitination; IDA.
DR   GO; GO:0007089; P:traversing start control point of mitotic c. . .; IDA.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB_MDM2.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
SQ   SEQUENCE   489 AA;  54557 MW;  4ABF489A82038DF4 CRC64;

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  Best Local Similarity  82.6%;  Pred. No. 1.4e-36;
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Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              |||||||||| ||||| |||||||||| |||||||:: |:||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQNDTYTMKEIIFYIGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
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Db         77 CSNDLLGDVFGVPSFSVKEHRKIYAMIYRNLVAVSQQ---DSGTSLSES 122


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AC   Q8WYJ3;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   MDM2 protein (Fragment).
GN   Name=MDM2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21248713; PubMed=11351297;
RA   Tamborini E., Della Torre G., Lavarino C., Azzarelli A.,
RA   Carpinelli P., Pierotti M.A., Pilotti S.;
RT   "Analysis of the molecular species generated by MDM2 gene
RT   amplification in liposarcomas.";
RL   Int. J. Cancer 92:790-796(2001).
DR   EMBL; AF092843; AAL40178.1; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB_MDM2.
DR   Pfam; PF02201; SWIB; 1.
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SQ   SEQUENCE   118 AA;  13536 MW;  D7A4DBAA83D8841B CRC64;

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Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVV 93
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RESULT 15
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ID   MDM2_MESAU     STANDARD;      PRT;   466 AA.
AC   Q60524;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein
DE   Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Fragment).
GN   Name=MDM2;
OS   Mesocricetus auratus (Golden hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC   Mesocricetus.
OX   NCBI_TaxID=10036;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pancreas;
RX   MEDLINE=95300112; PubMed=7780969;
RA   Chang K.W., Laconi S., Mangold K.A., Hubchak S., Scarpelli D.G.;
RT   "Multiple genetic alterations in hamster pancreatic ductal
RT   adenocarcinomas.";
RL   Cancer Res. 55:2560-2568(1995).
CC   -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC       apoptosis by binding its transcriptional activation domain.
CC       Functions as a ubiquitin ligase E3, in the presence of E1 and E2,
CC       toward p53 and itself. Permits the nuclear export of p53 and
```

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CC       targets it for proteasome-mediated proteolysis (By similarity).
CC   -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity (By
CC       similarity).
CC   -!- SUBUNIT: Binds p53, p73, ARF(P14), ribosomal protein L5 and
CC       specifically to RNA. Can interact also with retinoblastoma protein
CC       (RB), E1A-associated protein EP300 and the E2F1 transcription
CC       factor (By similarity).
CC   -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed
CC       predominantly in the nucleoplasm (By similarity).
CC   -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its
CC       G1 arrest and apoptosis functions. It also binds p73 and E2F1.
CC       Region II contains most of a central acidic region required for
CC       interaction with ribosomal protein L5 and a putative C4-type zinc
CC       finger. The RING finger domain which coordinates two molecules of
CC       zinc interacts specifically with RNA whether or not zinc is
CC       present and mediates the hetero-oligomerization with MDM4. It is
CC       also essential for its ubiquitin ligase E3 activity toward p53 and
CC       itself (By similarity).
CC   -!- DISEASE: The gene for this protein is overexpressed in some
CC       tumors.
CC   -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.
CC   -!- SIMILARITY: Contains 1 RanBP2-type zinc finger.
CC   -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC   -!- SIMILARITY: Contains 1 SWIB domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
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DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Ligase; Metal-binding; Nuclear protein; Proto-oncogene;
KW   Ubl conjugation pathway; Zinc; Zinc-finger.
FT   NON_TER       1      1
FT   DOMAIN       19     98       SWIB.
FT   DOMAIN      169    175       Nuclear localization signal (Potential).
FT   DOMAIN      176    188       Nuclear export signal.
FT   DOMAIN      196    201       Poly-Ser.
FT   DOMAIN      196    290       ARF-binding.
FT   DOMAIN      228    317       Region II.
FT   DOMAIN      209    287       Asp/Glu-rich (acidic).
FT   ZN_FING     285    314       RanBP2-type.
FT   ZN_FING     419    460       RING-type.
FT   DOMAIN      447    454       Nucleolar localization signal
FT                                (Potential).
FT   NON_TER     466    466
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Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
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GenCore version 5.1.6

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Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	511	92.2	188	4	US-09-603-052-4	Sequence 4, Appli
2	511	92.2	491	1	US-07-903-103-2	Sequence 2, Appli
3	511	92.2	491	1	US-08-044-619A-2	Sequence 2, Appli
4	511	92.2	491	1	US-08-283-911-2	Sequence 2, Appli
5	511	92.2	491	1	US-08-245-500A-3	Sequence 3, Appli
6	511	92.2	491	1	US-08-390-546-3	Sequence 3, Appli
7	511	92.2	491	1	US-08-390-479A-3	Sequence 3, Appli
8	511	92.2	491	1	US-08-557-393-3	Sequence 3, Appli
9	511	92.2	491	1	US-08-390-516C-3	Sequence 3, Appli
10	511	92.2	491	1	US-08-390-517A-3	Sequence 3, Appli
11	511	92.2	491	1	US-08-390-515A-3	Sequence 3, Appli
12	511	92.2	491	2	US-08-801-718-3	Sequence 3, Appli
13	511	92.2	491	3	US-09-170-159A-3	Sequence 3, Appli
14	511	92.2	491	4	US-09-480-718-44	Sequence 44, Appl
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16	451.5	81.5	489	1	US-07-903-103-4	Sequence 4, Appli
17	451.5	81.5	489	1	US-08-044-619A-4	Sequence 4, Appli
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19	451.5	81.5	489	1	US-08-245-500A-5	Sequence 5, Appli
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21	451.5	81.5	489	1	US-08-390-479A-5	Sequence 5, Appli
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28	451.5	81.5	489	4	US-09-480-718-46	Sequence 46, Appl
29	164	29.6	243	4	US-09-786-702-2	Sequence 2, Appli
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31	68	12.3	1432	3	US-08-781-891-71	Sequence 71, Appl
32	68	12.3	1432	4	US-09-618-166-71	Sequence 71, Appl
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34	67	12.1	206	3	US-09-311-311C-22	Sequence 22, Appl
35	67	12.1	418	1	US-08-224-930-4	Sequence 4, Appli
36	67	12.1	418	3	US-08-908-436-6	Sequence 6, Appli
37	67	12.1	418	3	US-09-561-756-18	Sequence 18, Appl
38	67	12.1	418	3	US-09-227-721-18	Sequence 18, Appl
39	67	12.1	418	4	US-09-954-697-18	Sequence 18, Appl
40	66.5	12.0	198	3	US-09-213-293D-10	Sequence 10, Appl
41	66.5	12.0	550	4	US-09-075-505-7	Sequence 7, Appli
42	66.5	12.0	816	1	US-08-038-760-3	Sequence 3, Appli
43	66.5	12.0	816	2	US-08-470-091-3	Sequence 3, Appli
44	66.5	12.0	928	1	US-08-204-329-1	Sequence 1, Appli
45	66.5	12.0	928	2	US-08-959-638-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-603-052-4
; Sequence 4, Application US/09603052
; Patent No. 6492116
; GENERAL INFORMATION:
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; TITLE OF INVENTION: Assay for identifying inhibitors of the interaction
; TITLE OF INVENTION: between proteins p53 and dm2
; FILE REFERENCE: MEWB26.001C1
; CURRENT APPLICATION NUMBER: US/09/603,052
; CURRENT FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: EP 95810576.9
; PRIOR FILING DATE: 1995-09-18
; PRIOR APPLICATION NUMBER: PCT/EP96/03957
; PRIOR FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-603-052-4

Query Match 92.2%; Score 511; DB 4; Length 188;
Best Local Similarity 94.5%; Pred. No. 8e-54;
Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
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Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||  |||||||  ||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125
```

RESULT 2
US-07-903-103-2
; Sequence 2, Application US/07903103
; Patent No. 5411860
; GENERAL INFORMATION:
; APPLICANT: VOGELSTEIN, BERT
; APPLICANT: KINZLER, KENNETH
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G ST., N.W.

```
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001-4597
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/903,103
;      FILING DATE:  19920623
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/867.840
;      FILING DATE:  07-APR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.40148
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-903-103-2

  Query Match             92.2%;  Score 511;  DB 1;  Length 491;
  Best Local Similarity   94.5%;  Pred. No. 2.8e-53;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              |||||||||| ||||| |||||||||||||||||| ||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 3
US-08-044-619A-2
; Sequence 2, Application US/08044619A
; Patent No. 5420263
;  GENERAL INFORMATION:
;    APPLICANT:  THE JOHNS HOPKINS UNIVERSITY
;    APPLICANT:  720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G ST., N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001-4597
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/044,619A
;      FILING DATE:  07-APR-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/903,103
;      FILING DATE:  23-JUN-1992
;      APPLICATION NUMBER:  US 07/867.840
;      FILING DATE:  07-APR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.40148
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-044-619A-2

  Query Match             92.2%;  Score 511;  DB 1;  Length 491;
  Best Local Similarity   94.5%;  Pred. No. 2.8e-53;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              |||||||||| ||||| |||||||||||||||||| ||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 4
US-08-283-911-2
; Sequence 2, Application US/08283911
; Patent No. 5519118
;  GENERAL INFORMATION:
;    APPLICANT:  VOGELSTEIN, BERT
;    APPLICANT:  KINZLER, KENNETH
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G ST., N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001-4597
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/283,911
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/903,103
;      FILING DATE:  23-JUN-1992
;      APPLICATION NUMBER:  US 07/867.840
;      FILING DATE:  07-APR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.40148
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-283-911-2

  Query Match             92.2%;  Score 511;  DB 1;  Length 491;
  Best Local Similarity   94.5%;  Pred. No. 2.8e-53;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 5
US-08-245-500A-3
; Sequence 3, Application US/08245500A
; Patent No. 5550023
;  GENERAL INFORMATION:
;    APPLICANT:  BURRELL, MARILEE
;    APPLICANT:  HILL, DAVID E.
;    APPLICANT:  KINZLER, KENNETH W.
;    APPLICANT:  VOGELSTEIN, BERT
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/245,500A
;      FILING DATE:  07-APR-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.42798
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-245-500A-3

  Query Match             92.2%;  Score 511;  DB 1;  Length 491;
  Best Local Similarity   94.5%;  Pred. No. 2.8e-53;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 6
US-08-390-546-3
; Sequence 3, Application US/08390546
; Patent No. 5606044
;  GENERAL INFORMATION:
;    APPLICANT:  BURRELL, MARILEE
;    APPLICANT:  HILL, DAVID E.
;    APPLICANT:  KINZLER, KENNETH W.
;    APPLICANT:  VOGELSTEIN, BERT
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/390,546
;      FILING DATE:  07-APR-1993
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.42798
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-390-546-3

  Query Match             92.2%;  Score 511;  DB 1;  Length 491;
  Best Local Similarity   94.5%;  Pred. No. 2.8e-53;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 7
US-08-390-479A-3
; Sequence 3, Application US/08390479A
; Patent No. 5618921
;  GENERAL INFORMATION:
;    APPLICANT:  BURRELL, MARILEE
;    APPLICANT:  HILL, DAVID E.
;    APPLICANT:  KINZLER, KENNETH W.
;    APPLICANT:  VOGELSTEIN, BERT
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
```

```
;      ADDRESSEE:  BANNER & WITCOFF, LTD.
;      STREET:  1001 G STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/390,479A
;      FILING DATE:  02-FEB-1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.48992
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-390-479A-3

  Query Match             92.2%;  Score 511;  DB 1;  Length 491;
  Best Local Similarity   94.5%;  Pred. No. 2.8e-53;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              ||||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 8
US-08-557-393-3
; Sequence 3, Application US/08557393
; Patent No. 5702903
;  GENERAL INFORMATION:
;    APPLICANT:  BURRELL, MARILEE
;    APPLICANT:  HILL, DAVID E.
;    APPLICANT:  KINZLER, KENNETH W.
;    APPLICANT:  VOGELSTEIN, BERT
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/557,393
;      FILING DATE:  13-NOV-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/245,500
;      FILING DATE:  18-MAY-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.42798
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-557-393-3

  Query Match             92.2%;  Score 511;  DB 1;  Length 491;
  Best Local Similarity   94.5%;  Pred. No. 2.8e-53;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              ||||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 9
US-08-390-516C-3
; Sequence 3, Application US/08390516C
; Patent No. 5708136
;  GENERAL INFORMATION:
;    APPLICANT:  BURRELL, MARILEE
;    APPLICANT:  HILL, DAVID E.
;    APPLICANT:  KINZLER, KENNETH W.
;    APPLICANT:  VOGELSTEIN, BERT
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/390,516C
;      FILING DATE:  07-APR-1993
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.42798
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
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US-08-390-516C-3

  Query Match             92.2%;  Score 511;  DB 1;  Length 491;
  Best Local Similarity   94.5%;  Pred. No. 2.8e-53;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 10
US-08-390-517A-3
; Sequence 3, Application US/08390517A
; Patent No. 5736338
;  GENERAL INFORMATION:
;    APPLICANT:  BURRELL, MARILEE
;    APPLICANT:  HILL, DAVID E.
;    APPLICANT:  KINZLER, KENNETH W.
;    APPLICANT:  VOGELSTEIN, BERT
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/390,517A
;      FILING DATE:  07-APR-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.42798
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-390-517A-3

  Query Match             92.2%;  Score 511;  DB 1;  Length 491;
  Best Local Similarity   94.5%;  Pred. No. 2.8e-53;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
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Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 11
US-08-390-515A-3
; Sequence 3, Application US/08390515A
; Patent No. 5756455
;  GENERAL INFORMATION:
;    APPLICANT:  BURRELL, MARILEE
;    APPLICANT:  HILL, DAVID E.
;    APPLICANT:  KINZLER, KENNETH W.
;    APPLICANT:  VOGELSTEIN, BERT
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/390,515A
;      FILING DATE:  07-APR-1993
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.42798
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-390-515A-3

  Query Match             92.2%;  Score 511;  DB 1;  Length 491;
  Best Local Similarity   94.5%;  Pred. No. 2.8e-53;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
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Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 12
US-08-801-718-3
; Sequence 3, Application US/08801718
; Patent No. 5858976
;  GENERAL INFORMATION:
;    APPLICANT:  BURRELL, MARILEE
;    APPLICANT:  HILL, DAVID E.
;    APPLICANT:  KINZLER, KENNETH W.
;    APPLICANT:  VOGELSTEIN, BERT
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
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;      COUNTRY:  USA
;      ZIP:  20001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/801,718
;      FILING DATE:  14-FEB-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/390,515
;      FILING DATE:  07-APR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.42798
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-801-718-3

  Query Match             92.2%;  Score 511;  DB 2;  Length 491;
  Best Local Similarity   94.5%;  Pred. No. 2.8e-53;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
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Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
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Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 13
US-09-170-159A-3
; Sequence 3, Application US/09170159A
; Patent No. 6399755
;   GENERAL INFORMATION:
;       APPLICANT: BURRELL, MARILEE
;                  HILL, DAVID E.
;                  KINZLER, KENNETH W.
;                  VOGELSTEIN, BERT
;       TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
;                           HUMAN TUMORS
;       NUMBER OF SEQUENCES: 5
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
;            STREET: 1001 G STREET, N.W.
;            CITY: WASHINGTON
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20001
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/170,159A
;            FILING DATE: 13-Oct-1998
;            CLASSIFICATION: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: KAGAN, SARAH A.
;            REGISTRATION NUMBER: 32,141
;            REFERENCE/DOCKET NUMBER: 01107.42798
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-508-9100
;            TELEFAX: 202-508-9299
;            TELEX: 197430 BBMB UT
;   INFORMATION FOR SEQ ID NO: 3:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 491 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-170-159A-3

  Query Match             92.2%;  Score 511;  DB 3;  Length 491;
  Best Local Similarity   94.5%;  Pred. No. 2.8e-53;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
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Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
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Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 14
US-09-480-718-44
; Sequence 44, Application US/09480718
; Patent No. 6407062
; GENERAL INFORMATION:
;  APPLICANT: Sherr, Charles J
;  APPLICANT: Quelle, Dawn E
;  APPLICANT: Weber, Jason D.
;  APPLICANT: Roussel, Martine F.
;  APPLICANT: Frederique, Zindy
;  TITLE OF INVENTION: ARF-19, A NOVEL REGULATOR OF THE MAMMALIAN CELL CYCLE
;  FILE REFERENCE: 1340-1-023 CIP 1
;  CURRENT APPLICATION NUMBER: US/09/480,718
;  CURRENT FILING DATE: 2000-01-07
;  EARLIER APPLICATION NUMBER: 09/129,855
;  EARLIER FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-480-718-44

  Query Match             92.2%;  Score 511;  DB 4;  Length 491;
  Best Local Similarity   94.5%;  Pred. No. 2.8e-53;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

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Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
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Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 15
US-09-510-252-4
; Sequence 4, Application US/09510252
; Patent No. 6372490
; GENERAL INFORMATION:
;  APPLICANT: Nandabalan, Krishnan
;  APPLICANT:  Yang, Meijia
;  APPLICANT:  Schulz, Vincent
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;  APPLICANT:  CuraGen Corporation
;  TITLE OF INVENTION: MDM INTERACTING PROTEIN AND METHODS OF USE THEREOF
;  FILE REFERENCE: 15966-524 MDM US
;  CURRENT APPLICATION NUMBER: US/09/510,252
;  CURRENT FILING DATE:  2000-02-22
;  PRIOR APPLICATION NUMBER: USSN 60/121,192
;  PRIOR FILING DATE: 1999-02-23
;  PRIOR APPLICATION NUMBER: USSN 60/122,643
;  PRIOR FILING DATE: 1999-03-03
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 216
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-510-252-4

  Query Match             89.3%;  Score 494.5;  DB 3;  Length 216;
  Best Local Similarity   93.6%;  Pred. No. 9.5e-52;
  Matches  102;  Conservative    0;  Mismatches    6;  Indels    1;  Gaps    1;

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:59:36 ; Search time 69.4 Seconds
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567.443 Million cell updates/sec

Title: US-10-822-254-12
Perfect score: 554
Sequence: 1 SQIPASEQETKVRPKPKLLK.....NLVVVNQQESSDSGTSVSEN 109

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Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	511	92.2	491	9	US-09-956-425-8	Sequence 8, Appli
3	511	92.2	491	10	US-09-029-327-2	Sequence 2, Appli
4	511	92.2	491	11	US-09-966-724-2	Sequence 2, Appli
5	511	92.2	491	15	US-10-422-536-137	Sequence 137, App
6	511	92.2	491	15	US-10-232-951-35	Sequence 35, Appl
7	511	92.2	491	17	US-10-685-838-1	Sequence 1, Appli
8	511	92.2	491	17	US-10-724-225-2	Sequence 2, Appli
9	511	92.2	491	17	US-10-489-802-8	Sequence 8, Appli
10	511	92.2	491	17	US-10-723-860-2236	Sequence 2236, Ap
11	494.5	89.3	216	13	US-10-057-510-4	Sequence 4, Appli
12	485.5	87.6	522	15	US-10-287-226-380	Sequence 380, App
13	485.5	87.6	522	15	US-10-287-226-382	Sequence 382, App
14	451.5	81.5	489	9	US-09-956-425-6	Sequence 6, Appli
15	451.5	81.5	489	11	US-09-966-724-4	Sequence 4, Appli
16	451.5	81.5	489	17	US-10-489-802-6	Sequence 6, Appli
17	444	80.1	95	17	US-10-685-838-2	Sequence 2, Appli
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19	431	77.8	92	17	US-10-685-838-3	Sequence 3, Appli
20	284	51.3	59	14	US-10-211-088-143	Sequence 143, App
21	83	15.0	269	17	US-10-425-115-360814	Sequence 360814,
22	83	15.0	281	15	US-10-425-114-57869	Sequence 57869, A
23	77.5	14.0	709	15	US-10-282-122A-63455	Sequence 63455, A
24	76.5	13.8	328	17	US-10-425-115-191466	Sequence 191466,
25	76.5	13.8	337	14	US-10-369-493-6239	Sequence 6239, Ap
26	75.5	13.6	291	15	US-10-425-114-59572	Sequence 59572, A
27	75.5	13.6	291	17	US-10-425-115-191465	Sequence 191465,
28	74	13.4	701	15	US-10-282-122A-53065	Sequence 53065, A
29	72.5	13.1	331	16	US-10-755-889-520	Sequence 520, App
30	72.5	13.1	479	14	US-10-050-704-231	Sequence 231, App
31	72.5	13.1	479	16	US-10-798-512-231	Sequence 231, App
32	72.5	13.1	559	14	US-10-050-704-111	Sequence 111, App
33	72.5	13.1	559	16	US-10-798-512-111	Sequence 111, App
34	72.5	13.1	568	14	US-10-295-027-1218	Sequence 1218, Ap
35	72	13.0	438	14	US-10-176-584A-2	Sequence 2, Appli
36	72	13.0	755	14	US-10-369-493-1985	Sequence 1985, Ap
37	71.5	12.9	332	15	US-10-425-114-47234	Sequence 47234, A
38	71.5	12.9	525	16	US-10-437-963-113360	Sequence 113360,
39	71.5	12.9	2932	16	US-10-437-963-120244	Sequence 120244,
40	71	12.8	1089	14	US-10-032-585-7664	Sequence 7664, Ap
41	71	12.8	1448	16	US-10-437-963-138597	Sequence 138597,
42	70.5	12.7	241	14	US-10-104-047-2203	Sequence 2203, Ap
43	70.5	12.7	293	16	US-10-473-670-10	Sequence 10, Appl
44	70.5	12.7	536	17	US-10-723-860-3919	Sequence 3919, Ap
45	70.5	12.7	821	16	US-10-437-963-110602	Sequence 110602,

ALIGNMENTS

RESULT 1
US-09-888-077-1
; Sequence 1, Application US/09888077
; Patent No. US20020031818A1
; GENERAL INFORMATION:
; APPLICANT: Ronai, Ze'ev
; APPLICANT: Fuchs, Serge
; TITLE OF INVENTION: Modification of Mdm2 Activity
; FILE REFERENCE: 2420/1H195-US1
; CURRENT APPLICATION NUMBER: US/09/888,077
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,343
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-888-077-1

Query Match 92.2%; Score 511; DB 9; Length 491;
Best Local Similarity 94.5%; Pred. No. 1.7e-47;
Matches 103; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
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Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
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RESULT 2
US-09-956-425-8

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; Sequence 8, Application US/09956425
; Patent No. US20020045192A1
; GENERAL INFORMATION:
;  APPLICANT: Kriwacki, Richard
;  APPLICANT:  Bothner, Brian
;  APPLICANT:  Lewis, William
;  TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and Method of Use Thereof
;  FILE REFERENCE: 1340/1/035
;  CURRENT APPLICATION NUMBER: US/09/956,425
;  CURRENT FILING DATE:  2001-09-19
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-956-425-8

  Query Match             92.2%;  Score 511;  DB 9;  Length 491;
  Best Local Similarity   94.5%;  Pred. No. 1.7e-47;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

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Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 3
US-09-029-327-2
; Sequence 2, Application US/09029327
; Publication No. US20030060432A1
;  GENERAL INFORMATION:
;    APPLICANT:  TOCQUE, Bruno
;    APPLICANT:  WASYLYK, Bohdan
;    APPLICANT:  DUBS-POTERSZMAN,
;    APPLICANT:  Marie-Christine
;    TITLE OF INVENTION:  ANTAGONISTS OF THE ONCOGENIC ACTIVITY OF
;    TITLE OF INVENTION:  THE PROTEIN MDM2, AND USE THEREOF IN THE TREATMENT OF
;    TITLE OF INVENTION:  CANCERS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rhone-Poulenc Rorer Inc.
;      STREET:  500 Arcola Road, Mailstop 3C43
;      CITY:  Collegeville
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19426
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/029,327
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR 96/01340
;      FILING DATE:  02-SEP-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO FR95/10331
;      FILING DATE:  04-SEP-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fehlner Esq., Paul F.
;      REGISTRATION NUMBER:  35,135
;      REFERENCE/DOCKET NUMBER:  ST95050-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (610) 454-3839
;      TELEFAX:  (610) 454-3808
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-029-327-2

  Query Match             92.2%;  Score 511;  DB 10;  Length 491;
  Best Local Similarity   94.5%;  Pred. No. 1.7e-47;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              ||||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 4
US-09-966-724-2
; Sequence 2, Application US/09966724
; Publication No. US20040170971A1
;  GENERAL INFORMATION:
;       APPLICANT: THE JOHNS HOPKINS UNIVERSITY
;                  720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA
;       TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
;                           HUMAN TUMORS
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
;            STREET: 1001 G ST., N.W.
;            CITY: WASHINGTON
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20001-4597
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/966,724
;            FILING DATE: 01-Oct-2001
;            CLASSIFICATION: 435
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/044,619
;            FILING DATE: 2001-10-01
;            APPLICATION NUMBER: US 07/867.840
;            FILING DATE: 07-APR-1992
;       ATTORNEY/AGENT INFORMATION:
;            NAME: KAGAN, SARAH A.
;            REGISTRATION NUMBER: 32,141
;            REFERENCE/DOCKET NUMBER: 01107.40148
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-508-9100
;            TELEFAX: 202-508-9299
;            TELEX: 197430 BBMB UT
;  INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 491 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-966-724-2

  Query Match             92.2%;  Score 511;  DB 11;  Length 491;
  Best Local Similarity   94.5%;  Pred. No. 1.7e-47;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;
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```
Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 5
US-10-422-536-137
; Sequence 137, Application US/10422536
; Publication No. US20040014100A1
; GENERAL INFORMATION:
;  APPLICANT: Kinsella, Todd
;  APPLICANT:  Lorens, James
;  APPLICANT:  Pray, Todd
;  APPLICANT:  Bennett, Mark
;  TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR INHIBITING
;  TITLE OF INVENTION:  PROTEIN-PROTEIN INTERACTION
;  FILE REFERENCE: A-71433-1/AMP/CYO
;  CURRENT APPLICATION NUMBER: US/10/422,536
;  CURRENT FILING DATE:  2003-04-23
;  PRIOR APPLICATION NUMBER: US 60/187,130
;  PRIOR FILING DATE: 2000-03-06
;  PRIOR APPLICATION NUMBER: US 09/800,770
;  PRIOR FILING DATE: 2001-03-06
;  PRIOR APPLICATION NUMBER: US 10/232,758
;  PRIOR FILING DATE: 2002-08-30
;  NUMBER OF SEQ ID NOS: 168
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 137
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-422-536-137

  Query Match             92.2%;  Score 511;  DB 15;  Length 491;
  Best Local Similarity   94.5%;  Pred. No. 1.7e-47;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 6
US-10-232-951-35
; Sequence 35, Application US/10232951
; Publication No. US20040043386A1
; GENERAL INFORMATION:
;  APPLICANT: Pray, Todd
;  APPLICANT:  Wong, Brian
;  APPLICANT:  Bennett, Mark
;  APPLICANT:  Parlati, Francesco
;  APPLICANT:  Rigel Pharmaceuticals, Incorporated
;  TITLE OF INVENTION: Methods and Compositions for Functional Ubiquitin
;  TITLE OF INVENTION:  Assays
;  FILE REFERENCE: 021044-006800US
;  CURRENT APPLICATION NUMBER: US/10/232,951
;  CURRENT FILING DATE:  2002-08-30
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: E3 ubiquitin ligating agent mouse double minute 2
;   OTHER INFORMATION: (mdm2) homolog full length protein isoform, mouse
;   OTHER INFORMATION: p53-binding protein (MDM2) homolog, transcript
;   OTHER INFORMATION: variant MDM2, transformed 3T3 cell double minute 2,
;   OTHER INFORMATION: Mdm2 cDNA
US-10-232-951-35

  Query Match             92.2%;  Score 511;  DB 15;  Length 491;
  Best Local Similarity   94.5%;  Pred. No. 1.7e-47;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 7
US-10-685-838-1
; Sequence 1, Application US/10685838
; Publication No. US20040197893A1
; GENERAL INFORMATION:
;  APPLICANT: SHUBERT, CARSTEN
;  APPLICANT:  GRASBERGER, BRUCE
;  APPLICANT:  MAGUIRE, DIANE
;  APPLICANT:  DECKMAN, INGRID
;  APPLICANT:  SPURLINO, JOHN
;  TITLE OF INVENTION: HDM2-INHIBITOR COMPLEXES AND USES THEREOF
;  FILE REFERENCE: PRD-2137-USANP
;  CURRENT APPLICATION NUMBER: US/10/685,838
;  CURRENT FILING DATE:  2003-10-15
;  PRIOR APPLICATION NUMBER: 60/418,350
;  PRIOR FILING DATE: 2002-10-16
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-685-838-1

  Query Match             92.2%;  Score 511;  DB 17;  Length 491;
  Best Local Similarity   94.5%;  Pred. No. 1.7e-47;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 8
US-10-724-225-2
; Sequence 2, Application US/10724225
; Publication No. US20040209834A1
;   GENERAL INFORMATION:
;        APPLICANT: TOCQUE, Bruno
;                   WASYLYK, Bohdan
;                   DUBS-POTERSZMAN,
;                   Marie-Christine
;        TITLE OF INVENTION: ANTAGONISTS OF THE ONCOGENIC ACTIVITY OF
;                            THE PROTEIN MDM2, AND USE THEREOF IN THE TREATMENT OF
;                            CANCERS
;        NUMBER OF SEQUENCES: 4
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Rhone-Poulenc Rorer Inc.
;             STREET: 500 Arcola Road, Mailstop 3C43
;             CITY: Collegeville
```

```
;            STATE: PA
;            COUNTRY: USA
;            ZIP: 19426
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/724,225
;            FILING DATE: 01-Dec-2003
;            CLASSIFICATION: 514
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/029,327
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: FR 96/01340
;            FILING DATE: 02-SEP-1996
;            APPLICATION NUMBER: WO FR95/10331
;            FILING DATE: 04-SEP-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Fehlner Esq., Paul F.
;            REGISTRATION NUMBER: 35,135
;            REFERENCE/DOCKET NUMBER: ST95050-US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (610) 454-3839
;            TELEFAX: (610) 454-3808
;   INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 491 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-724-225-2

  Query Match            92.2%;  Score 511;  DB 17;  Length 491;
  Best Local Similarity  94.5%;  Pred. No. 1.7e-47;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 9
US-10-489-802-8
; Sequence 8, Application US/10489802
; Publication No. US20040248198A1
; GENERAL INFORMATION:
;  APPLICANT: St. Jude Children's Research Hospital, Inc.
;  APPLICANT:  Kriwacki, Richard
;  APPLICANT:  Bothner, Brian
;  APPLICANT:  Lewis, William
;  TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and
;  TITLE OF INVENTION:  Method of Use Thereof
;  FILE REFERENCE: 44158/243642
;  CURRENT APPLICATION NUMBER: US/10/489,802
;  CURRENT FILING DATE:  2004-03-16
;  PRIOR APPLICATION NUMBER: US 09/956,425
;  PRIOR FILING DATE: 2001-09-19
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-489-802-8

  Query Match            92.2%;  Score 511;  DB 17;  Length 491;
  Best Local Similarity  94.5%;  Pred. No. 1.7e-47;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 10
US-10-723-860-2236
; Sequence 2236, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
;  APPLICANT: Aziz, Natasha
;  APPLICANT:  Ginsburg, Wendy M.
;  APPLICANT:  Zlotnik, Albert
;  TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
;  TITLE OF INVENTION:  Methods for Screening for Soft Tissue Sarcoma Modulators
;  FILE REFERENCE: 05882.0193.NPUS01
;  CURRENT APPLICATION NUMBER: US/10/723,860
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: 60/429,739
;  PRIOR FILING DATE: 2002-11-26
;  NUMBER OF SEQ ID NOS: 8393
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2236
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-723-860-2236

  Query Match            92.2%;  Score 511;  DB 17;  Length 491;
  Best Local Similarity  94.5%;  Pred. No. 1.7e-47;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              |||||||||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| |||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 11
US-10-057-510-4
; Sequence 4, Application US/10057510
; Publication No. US20020098580A1
; GENERAL INFORMATION:
;  APPLICANT: Nandabalan, Krishnan
;  APPLICANT:  Yang, Meijia
;  APPLICANT:  Schulz, Vincent
;  APPLICANT:  CuraGen Corporation
;  TITLE OF INVENTION: MDM INTERACTING PROTEIN AND METHODS OF USE THEREOF
;  FILE REFERENCE: 15966-524 MDM US
;  CURRENT APPLICATION NUMBER: US/10/057,510
;  CURRENT FILING DATE:  2002-01-25
;  PRIOR APPLICATION NUMBER: USSN 09/510,252
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: USSN 60/121,192
;  PRIOR FILING DATE: 1999-02-23
;  PRIOR APPLICATION NUMBER: USSN 60/122,643
;  PRIOR FILING DATE: 1999-03-03
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 216
;   TYPE: PRT
;   ORGANISM: Homo sapiens
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US-10-057-510-4

  Query Match             89.3%;  Score 494.5;  DB 13;  Length 216;
  Best Local Similarity   93.6%;  Pred. No. 3.9e-46;
  Matches  102;  Conservative    0;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              |||||||||| ||||| |||||||||||||||||||| || ||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYL-QYIMTKRLYDEKQQHIVY 75

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| ||||||| ||||||||||||||||||||||||||||||||||||
Db         76 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 124


RESULT 12
US-10-287-226-380
; Sequence 380, Application US/10287226
; Publication No. US20040086875A1
; GENERAL INFORMATION:
;  APPLICANT: Agee, Michele L.,
;  APPLICANT:  Alsobrook, John P.,
;  APPLICANT:  Berghs, Constance,
;  APPLICANT:  Boldog, Ference,
;  APPLICANT:  Burgess, Catherine E.,
;  APPLICANT:  Chant, John S.,
;  APPLICANT:  Chaudhuri, Amitabha,
;  APPLICANT:  DiPippo, Vincent A.,
;  APPLICANT:  Edinger, Shlomit R.,
;  APPLICANT:  Eisen, Andrew,
;  APPLICANT:  Ellerman, Karen,
;  APPLICANT:  Gangolli, Esha A.,
;  APPLICANT:  Gorman, Linda,
;  APPLICANT:  Gerlach, Valerie,
;  APPLICANT:  Ji, Weizhen,
;  APPLICANT:  Kekuda, Ramesh,
;  APPLICANT:  Khramtsov, Nikolai,
;  APPLICANT:  Li, Li,
;  APPLICANT:  Malyankar, Uriel M.,
;  APPLICANT:  MacDougall, John R.,
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Miller, Charles E.,
;  APPLICANT:  Millet, Isabelle,
;  APPLICANT:  Ooi, Chean Eng,
;  APPLICANT:  Ort, Tatiana,
;  APPLICANT:  Padigaru, Muralidhara,
;  APPLICANT:  Patturajan, Meera,
;  APPLICANT:  Rastelli, Luca,
;  APPLICANT:  Rieger, Daniel K.,
;  APPLICANT:  Rothenberg, Mark E.,
;  APPLICANT:  Shenoy, Suresh G.,
;  APPLICANT:  Spaderna, Steven K.,
;  APPLICANT:  Spytek, Kimberley A.,
;  APPLICANT:  Taupier, Jr., Raymond J.,
;  APPLICANT:  Vernet, Corine A.M.,
;  APPLICANT:  Zerhusen, Bryan D.,
;  APPLICANT:  Zhong, Mei
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-480C
;  CURRENT APPLICATION NUMBER: US/10/287,226
;  CURRENT FILING DATE:  2002-11-04
;  PRIOR APPLICATION NUMBER: 60/334,421
;  PRIOR FILING DATE: 2001-11-30
;  PRIOR APPLICATION NUMBER: 60/354,392
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: 60/360,148
;  PRIOR FILING DATE: 2002-02-27
;  PRIOR APPLICATION NUMBER: 60/364,000
;  PRIOR FILING DATE: 2002-03-13
;  PRIOR APPLICATION NUMBER: 60/404,821
;  PRIOR FILING DATE: 2002-08-20
;  PRIOR APPLICATION NUMBER: 60/334,526
;  PRIOR FILING DATE: 2001-11-30
;  PRIOR APPLICATION NUMBER: 60/354,409
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: 60/364,227
;  PRIOR FILING DATE: 2002-03-13
;  PRIOR APPLICATION NUMBER: 60/334,027
;  PRIOR FILING DATE: 2001-11-28
;  PRIOR APPLICATION NUMBER: 60/331,641
;  PRIOR FILING DATE: 2001-11-20
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 673
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 380
;   LENGTH: 522
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-287-226-380

  Query Match             87.6%;  Score 485.5;  DB 15;  Length 522;
  Best Local Similarity   73.6%;  Pred. No. 1.2e-44;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels   31;  Gaps    1;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKE---------------------- 36
              |||||||||| ||||| ||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKERWSFTMLPRLVWNSWAQGICLPRP 76

Qy         37 -------VLHYLGQYIMTKRLYDEKQQHIVKCSNDKLGDLFGVKSFSVKEHRKIYTMIYR 89
                    || |||||||||||||||||||| |||| ||||||| ||||||||||||||||
Db         77 PKVLDLQVLFYLGQYIMTKRLYDEKQQHIVYCSNDLLGDLFGVPSFSVKEHRKIYTMIYR 136

Qy         90 NLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||
Db        137 NLVVVNQQESSDSGTSVSEN 156


RESULT 13
US-10-287-226-382
; Sequence 382, Application US/10287226
; Publication No. US20040086875A1
; GENERAL INFORMATION:
;  APPLICANT: Agee, Michele L.,
;  APPLICANT:  Alsobrook, John P.,
;  APPLICANT:  Berghs, Constance,
;  APPLICANT:  Boldog, Ference,
;  APPLICANT:  Burgess, Catherine E.,
;  APPLICANT:  Chant, John S.,
;  APPLICANT:  Chaudhuri, Amitabha,
;  APPLICANT:  DiPippo, Vincent A.,
;  APPLICANT:  Edinger, Shlomit R.,
;  APPLICANT:  Eisen, Andrew,
;  APPLICANT:  Ellerman, Karen,
;  APPLICANT:  Gangolli, Esha A.,
;  APPLICANT:  Gorman, Linda,
;  APPLICANT:  Gerlach, Valerie,
;  APPLICANT:  Ji, Weizhen,
;  APPLICANT:  Kekuda, Ramesh,
;  APPLICANT:  Khramtsov, Nikolai,
;  APPLICANT:  Li, Li,
;  APPLICANT:  Malyankar, Uriel M.,
;  APPLICANT:  MacDougall, John R.,
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Miller, Charles E.,
;  APPLICANT:  Millet, Isabelle,
;  APPLICANT:  Ooi, Chean Eng,
;  APPLICANT:  Ort, Tatiana,
;  APPLICANT:  Padigaru, Muralidhara,
;  APPLICANT:  Patturajan, Meera,
;  APPLICANT:  Rastelli, Luca,
;  APPLICANT:  Rieger, Daniel K.,
;  APPLICANT:  Rothenberg, Mark E.,
;  APPLICANT:  Shenoy, Suresh G.,
;  APPLICANT:  Spaderna, Steven K.,
;  APPLICANT:  Spytek, Kimberley A.,
;  APPLICANT:  Taupier, Jr., Raymond J.,
```

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;  APPLICANT:  Vernet, Corine A.M.,
;  APPLICANT:  Zerhusen, Bryan D.,
;  APPLICANT:  Zhong, Mei
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-480C
;  CURRENT APPLICATION NUMBER: US/10/287,226
;  CURRENT FILING DATE:  2002-11-04
;  PRIOR APPLICATION NUMBER: 60/334,421
;  PRIOR FILING DATE: 2001-11-30
;  PRIOR APPLICATION NUMBER: 60/354,392
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: 60/360,148
;  PRIOR FILING DATE: 2002-02-27
;  PRIOR APPLICATION NUMBER: 60/364,000
;  PRIOR FILING DATE: 2002-03-13
;  PRIOR APPLICATION NUMBER: 60/404,821
;  PRIOR FILING DATE: 2002-08-20
;  PRIOR APPLICATION NUMBER: 60/334,526
;  PRIOR FILING DATE: 2001-11-30
;  PRIOR APPLICATION NUMBER: 60/354,409
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: 60/364,227
;  PRIOR FILING DATE: 2002-03-13
;  PRIOR APPLICATION NUMBER: 60/334,027
;  PRIOR FILING DATE: 2001-11-28
;  PRIOR APPLICATION NUMBER: 60/331,641
;  PRIOR FILING DATE: 2001-11-20
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 673
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 382
;   LENGTH: 522
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-287-226-382

  Query Match             87.6%;  Score 485.5;  DB 15;  Length 522;
  Best Local Similarity   73.6%;  Pred. No. 1.2e-44;
  Matches  103;  Conservative    0;  Mismatches    6;  Indels   31;  Gaps    1;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKE---------------------- 36
              |||||||||| ||||| ||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKERWSFTMLPRLVWNSWAQGICLPRP 76

Qy         37 -------VLHYLGQYIMTKRLYDEKQQHIVKCSNDKLGDLFGVKSFSVKEHRKIYTMIYR 89
                   || |||||||||||||||||||| |||| ||||||| ||||||||||||||||
Db         77 PKVLDLQVLFYLGQYIMTKRLYDEKQQHIVYCSNDLLGDLFGVPSFSVKEHRKIYTMIYR 136

Qy         90 NLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||
Db        137 NLVVVNQQESSDSGTSVSEN 156


RESULT 14
US-09-956-425-6
; Sequence 6, Application US/09956425
; Patent No. US20020045192A1
; GENERAL INFORMATION:
;  APPLICANT: Kriwacki, Richard
;  APPLICANT:  Bothner, Brian
;  APPLICANT:  Lewis, William
;  TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and Method of Use Thereof
;  FILE REFERENCE: 1340/1/035
;  CURRENT APPLICATION NUMBER: US/09/956,425
;  CURRENT FILING DATE:  2001-09-19
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 489
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-956-425-6

  Query Match             81.5%;  Score 451.5;  DB 9;  Length 489;
  Best Local Similarity   82.6%;  Pred. No. 5.9e-41;
  Matches   90;  Conservative    7;  Mismatches    9;  Indels    3;  Gaps    1;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              |||||||||| ||||| |||||||||| |||||||:: |:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQNDTYTMKEIIFYIGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| |||:||| |||||||||| ||||||| |:||   |||||:||:
Db         77 CSNDLLGDVFGVPSFSVKEHRKIYAMIYRNLVAVSQQ---DSGTSLSES 122


RESULT 15
US-09-966-724-4
; Sequence 4, Application US/09966724
; Publication No. US20040170971A1
;  GENERAL INFORMATION:
;       APPLICANT: THE JOHNS HOPKINS UNIVERSITY
;                  720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA
;       TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
;                           HUMAN TUMORS
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
;            STREET: 1001 G ST., N.W.
;            CITY: WASHINGTON
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20001-4597
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/966,724
;            FILING DATE: 01-Oct-2001
;            CLASSIFICATION: 435
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/044,619
;            FILING DATE: 2001-10-01
;            APPLICATION NUMBER: US 07/867.840
;            FILING DATE: 07-APR-1992
;       ATTORNEY/AGENT INFORMATION:
;            NAME: KAGAN, SARAH A.
;            REGISTRATION NUMBER: 32,141
;            REFERENCE/DOCKET NUMBER: 01107.40148
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-508-9100
;            TELEFAX: 202-508-9299
;            TELEX: 197430 BBMB UT
;   INFORMATION FOR SEQ ID NO: 4:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 489 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-966-724-4

  Query Match             81.5%;  Score 451.5;  DB 11;  Length 489;
  Best Local Similarity   82.6%;  Pred. No. 5.9e-41;
  Matches   90;  Conservative    7;  Mismatches    9;  Indels    3;  Gaps    1;

Qy          1 SQIPASEQETKVRPKPKLLKLLKSVGAQKDTYTMKEVLHYLGQYIMTKRLYDEKQQHIVK 60
              |||||||||| ||||| |||||||||| |||||||:: |:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQNDTYTMKEIIFYIGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDKLGDLFGVKSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||| |||:||| |||||||||| ||||||| |:||   |||||:||:
Db         77 CSNDLLGDVFGVPSFSVKEHRKIYAMIYRNLVAVSQQ---DSGTSLSES 122
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Search completed: January 27, 2005, 18:23:07
Job time : 70.4 secs

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:52:56 ; Search time 19.8 Seconds
(without alignments)
529.678 Million cell updates/sec

Title: US-10-822-254-8
Perfect score: 554
Sequence: 1 SQIPASEQETLVRPKPLLLK.....NLVVVNQQESSDSGTSVSEN 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	550	99.3	491	1	S24354	p53-binding protei
2	490.5	88.5	489	2	S15349	mdm2 protein - mou
3	279.5	50.5	489	2	S71955	MDM2-like p53-bind
4	77	13.9	685	1	SXBPT4	NAD+-protein ADP-r
5	77	13.9	698	1	S31630	NAD+-protein ADP-r
6	77	13.9	698	1	S31714	NAD+-protein ADP-r
7	76	13.7	967	2	A64710	type III restricti
8	72.5	13.1	565	2	S52682	hypothetical prote
9	72	13.0	969	2	E71810	type III restricti
10	71.5	12.9	401	2	F90288	hypothetical prote
11	71.5	12.9	422	2	T26334	hypothetical prote
12	71.5	12.9	514	2	D85069	hypothetical prote
13	71	12.8	206	1	XUBYMC	methylated-DNA-[pr
14	70.5	12.7	838	2	I45557	eyeless, long form
15	69.5	12.5	331	2	B84938	flagellar motor sw
16	69	12.5	181	2	S75415	probable ribosomal
17	68.5	12.4	277	2	AI0589	conserved hypothet
18	68.5	12.4	339	2	A90395	conserved hypothet
19	68	12.3	848	2	E86443	probable G-protein
20	68	12.3	860	2	S64366	hypothetical prote
21	67.5	12.2	517	2	S32169	hypothetical prote
22	67.5	12.2	709	2	E64213	DNA topoisomerase
23	67.5	12.2	1368	2	T18371	probable glutamate
24	67	12.1	170	2	T31967	hypothetical prote
25	67	12.1	261	2	H71680	exodeoxyribonuclea
26	67	12.1	1145	2	S55600	single-stranded DN
27	66.5	12.0	315	2	H81704	dipeptidase, proba
28	66.5	12.0	593	2	E81277	hypothetical prote
29	66.5	12.0	649	2	C81275	hypothetical prote
30	66.5	12.0	891	2	S27029	preprotein translo
31	66.5	12.0	1292	2	F64237	DNA-directed RNA p
32	66.5	12.0	2833	2	A43360	inositol 1,4,5-tri
33	66	11.9	1098	2	S38100	hypothetical prote
34	65.5	11.8	422	2	B95001	conserved domain p
35	65.5	11.8	445	2	A97873	conserved hypothet
36	65.5	11.8	447	2	I64002	sodium-translocati
37	65.5	11.8	455	2	S56695	1-aminocyclopropan
38	65.5	11.8	1268	2	T50252	probable transcrip
39	65	11.7	369	2	B70220	conserved hypothet
40	65	11.7	3092	2	S46009	GTPase-activating
41	65	11.7	3268	2	S69625	hypothetical prote
42	64.5	11.6	317	2	F97701	hypothetical prote
43	64.5	11.6	380	2	T32112	hypothetical prote
44	64.5	11.6	467	2	T25848	hypothetical prote
45	64.5	11.6	485	1	S19677	1-aminocyclopropan

ALIGNMENTS

RESULT 1
S24354
p53-binding protein mdm2 - human
N;Alternate names: mdm-2 oncogene; mouse double minute 2 homolog; p53-associated phospho
N;Contains: p53-binding protein mdm2, splice form A
C;Species: Homo sapiens (man)
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C;Accession: S24354; S57338; G02026
R;Oliner, J.D.; Kinzler, K.W.; Meltzer, P.S.; George, D.L.; Vogelstein, B.
Nature 358, 80-83, 1992
A;Title: Amplification of a gene encoding a p53-associated protein in human sarcomas.
A;Reference number: S24354; MUID:92310576; PMID:1614537
A;Accession: S24354
A;Molecule type: mRNA
A;Residues: 1-491 <OLI>
A;Cross-references: EMBL:Z12020; NID:g35211; PIDN:CAA78055.1; PID:g35212
R;Zauberman, A.; Flusberg, D.; Haupt, Y.; Barak, Y.; Oren, M.
Nucleic Acids Res. 23, 2584-2592, 1995
A;Title: A functional p53-responsive intronic promoter is contained within the human mdm
A;Reference number: S57338; MUID:95380270; PMID:7651818
A;Accession: S57338
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-16,'P',18-24 <ZAU>
A;Cross-references: EMBL:U28935; NID:g904033; PIDN:AAA82237.1; PID:g904034
R;Lunec, J.
submitted to the EMBL Data Library, August 1995
A;Description: Multiple alternate spliced mdm2 transcripts with loss of p53 binding doma
A;Reference number: G09070
A;Accession: G02026
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-27,223-491 <LUN>
A;Cross-references: EMBL:U33199; NID:g992676; PIDN:AAA75514.1; PID:g992677
A;Experimental source: splice form A
C;Genetics:
A;Gene: GDB:MDM2
A;Cross-references: GDB:250456; OMIM:164785
A;Map position: 12q14.3-12q15
C;Superfamily: human p53-binding protein mdm2
C;Keywords: alternative splicing; oncogene; phosphoprotein
F;1-491/Product: p53-binding protein mdm-2 #status predicted <MAT1>
F;1-27,223-491/Product: p53-binding protein mdm-2, splice form A #status predicted <MAT2

Query Match 99.3%; Score 550; DB 1; Length 491;
Best Local Similarity 99.1%; Pred. No. 1.7e-48;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76
```

```
Qy          61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125
```

RESULT 2
S15349
mdm2 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S15349
R;Fakharzadeh, S.S.; Trusko, S.P.; George, D.L.
EMBO J. 10, 1565-1569, 1991
A;Title: Tumorigenic potential associated with enhanced expression of a gene that is amp
A;Reference number: S15349; MUID:91224107; PMID:2026149
A;Accession: S15349
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-489 <FAK>
A;Cross-references: UNIPROT:P23804; EMBL:X58876; NID:g53038; PIDN:CAA41684.1; PID:g53039
C;Genetics:
A;Gene: mdm2
C;Superfamily: human p53-binding protein mdm2

```
  Query Match             88.5%;  Score 490.5;  DB 2;  Length 489;
  Best Local Similarity   87.2%;  Pred. No. 2.1e-42;
  Matches   95;  Conservative    8;  Mismatches    3;  Indels    3;  Gaps    1;

Qy           1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
               |||||||||||||||||||||||||| |||||||:::|:||||||||||||||||||||
Db          17 SQIPASEQETLVRPKPLLLKLLKSVGAQNDTYTMKEIIFYIGQYIMTKRLYDEKQQHIVY 76

Qy          61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
               ||||||||:|||||||||||||||| ||||||| |:||   |||||:||:
Db          77 CSNDLLGDVFGVPSFSVKEHRKIYAMIYRNLVAVSQQ---DSGTSLSES 122
```

RESULT 3
S71955
MDM2-like p53-binding protein MDMX - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
C;Accession: S71955
R;Shvarts, A.; Steegenga, W.T.; Riteco, N.; van Laar, T.; Dekker, P.; Bazuine, M.; van H
EMBO J. 15, 5349-5357, 1996
A;Title: MDMX: a novel p53-binding protein with some functional properties of MDM2.
A;Reference number: S71955; MUID:97050840; PMID:8895579
A;Accession: S71955
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-489 <SHV>
A;Cross-references: UNIPROT:O35618; EMBL:AF007110; NID:g2253388; PIDN:AAB62927.1; PID:g2
C;Genetics:
A;Gene: MDMX
C;Function:
A;Description: inhibits transcription activation function of tumour suppressor protein p
C;Superfamily: human p53-binding protein mdm2

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  Query Match             50.5%;  Score 279.5;  DB 2;  Length 489;
  Best Local Similarity   53.3%;  Pred. No. 8.1e-21;
  Matches   56;  Conservative   17;  Mismatches   21;  Indels   11;  Gaps    1;

Qy           5 ASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVYCSND 64
               :||| : |||| |||:| : ||| : :|||||::||||||| |:|||:::||:|||  |
Db          20 SSEQISQVRPKLQLLKILHAAGAQGEVFTMKEVMHYLGQYIMVKQLYDQQEQHMVYCGGD 79

Qy          65 LLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
               ||||| |  |||||:   :| |: :|||           || | |
Db          80 LLGDLLGCQSFSVKDPSPLYDMLRKNLV----------TSASNN 113
```

RESULT 4
SXBPT4
NAD+-protein ADP-ribosyltransferase (EC 2.4.2.-) precursor - phage T4
C;Species: phage T4
A;Note: host Escherichia coli
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C;Accession: JU0096
R;Hilse, D.; Koch, T.; Rueger, W.
Nucleic Acids Res. 17, 6731, 1989
A;Title: Nucleotide sequence of the alt gene of bacteriophage T4.
A;Reference number: JU0096; MUID:89386005; PMID:2506526
A;Accession: JU0096
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-685 <HIL>
A;Cross-references: UNIPROT:P12726
C;Comment: This enzyme catalyzes the ADP-ribosylation of one of the two alpha-subunits c
C;Genetics:
A;Gene: alt
C;Superfamily: phage T4 NAD-protein ADP-ribosyltransferase
C;Keywords: glycosyltransferase; pentosyltransferase
F;7-685/Product: NAD-protein ADP-ribosyltransferase #status predicted <MAT>

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  Query Match             13.9%;  Score 77;  DB 1;  Length 685;
  Best Local Similarity   28.0%;  Pred. No. 6.2;
  Matches   28;  Conservative   23;  Mismatches   35;  Indels   14;  Gaps    6;

Qy          18 LLKLLKS--VGAQKDTYTMKEVLYYL---GQYIMTKRL--YDEKQQHI-VYCSNDLLGDL 69
               :|::|||   |  :    : : |      |:|:: | |  ||:|  :| ::  |  | |:
Db         111 MLRILKSKTAGQARQIQVIADRLIRSRSGGRYVLLKELWDYDKKYAYILIHRKNVSLEDI 170

Qy          70 FGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
                |||  | :   |: : :    | :|:    |:|  |::|
Db         171 PGVPEISTELFTKVESKV--GDVYINK----DTGAQVTKN 204
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RESULT 5
S31630
NAD+-protein ADP-ribosyltransferase (EC 2.4.2.-) precursor - phage T2
C;Species: phage T2
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S31630
R;Koch, T.; Rueger, W.
submitted to the EMBL Data Library, December 1992
A;Description: The ADP-ribosyltransferase of bacteriophages T2, T4 and T6: Sequencing of
A;Reference number: S31630
A;Accession: S31630
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-698 <KOC>
A;Cross-references: UNIPROT:Q38424; EMBL:X69893; NID:g15187; PIDN:CAA49517.1; PID:g15188
C;Superfamily: phage T4 NAD-protein ADP-ribosyltransferase
C;Keywords: glycosyltransferase; NAD; pentosyltransferase

```
  Query Match             13.9%;  Score 77;  DB 1;  Length 698;
  Best Local Similarity   28.0%;  Pred. No. 6.4;
  Matches   28;  Conservative   23;  Mismatches   35;  Indels   14;  Gaps    6;

Qy          18 LLKLLKS--VGAQKDTYTMKEVLYYL---GQYIMTKRL--YDEKQQHI-VYCSNDLLGDL 69
               :|::|||   |  :    : : |      |:|:: | |  ||:|  :| ::  |  | |:
Db         112 MLRILKSKTAGQARQIQVIADRLIRSRSGGRYVLLKELWDYDKKYAYILIHRKNVSLEDI 171

Qy          70 FGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
                |||  | :   |: : :    | :|:    |:|  |::|
Db         172 PGVPEISTELFTKVESKV--GDVYINK----DTGAQVTKN 205
```

RESULT 6
S31714
NAD+-protein ADP-ribosyltransferase (EC 2.4.2.-) precursor - phage T6
C;Species: phage T6
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S31714
R;Koch, T.; Rueger, W.
submitted to the EMBL Data Library, December 1992

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A;Description: The ADP-ribosyltransferase of bacteriophages T2, T4 and T6: Sequencing of
A;Reference number: S31630
A;Accession: S31714
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-698 <KOC>
A;Cross-references: UNIPROT:Q38433; EMBL:X69894; NID:g15422; PIDN:CAA49518.1; PID:g15423
C;Superfamily: phage T4 NAD-protein ADP-ribosyltransferase
C;Keywords: glycosyltransferase; NAD; pentosyltransferase

  Query Match             13.9%;  Score 77;  DB 1;  Length 698;
  Best Local Similarity   28.0%;  Pred. No. 6.4;
  Matches   28;  Conservative   23;  Mismatches   35;  Indels   14;  Gaps    6;

Qy         18 LLKLLKS--VGAQKDTYTMKEVLYYL---GQYIMTKRL--YDEKQQHI-VYCSNDLLGDL 69
              :|::|||    |  :    : : |      |:|:: | |  ||:|  :| ::  |  | |:
Db        112 MLRILKSKTAGQARQIQVIADRLIRSRSGGRYVLLKELWDYDKKYAYILIHRKNVSLEDI 171

Qy         70 FGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
               |||  | :   |: : :    | :|:    |:|  |::|
Db        172 PGVPEISTELFTKVESKV--GDVYINK----DTGAQVTKN 205


RESULT 7
A64710
type III restriction enzyme R protein - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: A64710
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: A64710
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-967 <TOM>
A;Cross-references: UNIPROT:O26050; GB:AE000650; GB:AE000511; NID:g2314700; PIDN:AAD0856
C;Genetics:
A;Start codon: GTG

  Query Match             13.7%;  Score 76;  DB 2;  Length 967;
  Best Local Similarity   24.8%;  Pred. No. 12;
  Matches   26;  Conservative   22;  Mismatches   43;  Indels   14;  Gaps    3;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKR---LYDEKQQH 57
              ::|  :||| | | : | |:::      | :| |:|        |  ::    |||| :
Db        768 NEIKKNEQEGLRRLEELFLEIIYQNIKDKISYQMRETT------IKNRKNDAFYDEKGEI 821

Qy         58 IVYCSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDS 102
                :    |  | : : : ||:|       :| | : |: :   |:
Db        822 REFLDGSLGADKYEIKNSSVRE-----KCLYENFMQVDSEIEKDT 861


RESULT 8
S52682
hypothetical protein YDR117c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YD9727.12c
C;Species: Saccharomyces cerevisiae
C;Date: 19-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S52682
R;Murphy, L.; Shore, L.; Harris, D.
submitted to the EMBL Data Library, March 1995
A;Reference number: S52671
A;Accession: S52682
A;Molecule type: DNA
A;Residues: 1-565 <MUR>
A;Cross-references: UNIPROT:Q04600; EMBL:Z48758; NID:g747879; PID:g747891; GSPDB:GN00004
C;Genetics:
A;Gene: MIPS:YDR117c
A;Cross-references: SGD:S0002524
A;Map position: 4R

  Query Match             13.1%;  Score 72.5;  DB 2;  Length 565;
  Best Local Similarity   33.3%;  Pred. No. 14;
  Matches   25;  Conservative   11;  Mismatches   30;  Indels    9;  Gaps    3;

Qy         10 TLVRPKPLLLKLLKSVGAQKDT-YTMKEVLYYLGQYIMTKRLYDEKQQHIVYCSNDLLGD 68
              || :|  |   ||| |     | || :::   : |||  | | | | :  |   :||| |
Db        362 TLYKPFNLAKDLLKEVNLASHTYYTSQDIRSAVSQYISVKNLADTKDKGKV-IMDDLLFD 420

Qy         69 LFGVPSFSVKEHRKI 83
              :      | : :|:
Db        421 M-------VNKKKKV 428


RESULT 9
E71810
type III restriction enzyme - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: E71810
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.,
; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: E71810
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-969 <ARN>
A;Cross-references: UNIPROT:Q9ZJA3; GB:AE001563; GB:AE001439; NID:g4156027; PIDN:AAD0698
A;Experimental source: strain J99
C;Genetics:
A;Gene: res_2

  Query Match             13.0%;  Score 72;  DB 2;  Length 969;
  Best Local Similarity   23.8%;  Pred. No. 30;
  Matches   25;  Conservative   22;  Mismatches   44;  Indels   14;  Gaps    3;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKR---LYDEKQQH 57
              ::|  :||| | | : | |:::      | :| |:|        |  ::    |||| :
Db        770 NEIKKNEQEGLKRLEELFLEIIYQNIKDKISYQMRETT------IKNRKNDAFYDEKGEI 823

Qy         58 IVYCSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDS 102
                :    |  | : : : | :|       :| | : |: :   |:
Db        824 REFLDGSLGADKYEIKNSSAQE-----KCLYENFMQVDSEIEKDT 863


RESULT 10
F90288
hypothetical protein SSO1329 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: F90288
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: F90288
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-401 <KUR>
A;Cross-references: UNIPROT:Q97YJ4; GB:AE006641; NID:g13814535; PIDN:AAK41565.1; GSPDB:G
C;Genetics:
A;Gene: SSO1329

  Query Match             12.9%;  Score 71.5;  DB 2;  Length 401;
  Best Local Similarity   22.7%;  Pred. No. 12;
  Matches   27;  Conservative   22;  Mismatches   29;  Indels   41;  Gaps    7;
```

```
Qy          20 KLLKSVGAQK----DTYTMKEVLYYLGQYIMT----KRLYDEKQQHIVY------CSNDL 65
               |||  :    :    | ||:  : |||  |::|    :   | |:  : |       ||||
Db          27 KLLSTFNGTEEVPLDDYTLSYIYYYL-MYLITASVVRSAEDAKKSRLTYREFSIEYSNDL 85

Qy          66 LGDL---------------------FGVPSFSVKEH--RKIYTMI--YRNLVVVNQQE 98
                |:|                     :  | : :  :  |:||::|   |: : | :::
Db          86 YGELNVDLSIPVYSMGLVAYHSFTEGYNAPEYGILGYITRRIYSIIKEKRSKIEVRKEQ 144


RESULT 11
T26334
hypothetical protein W10G6.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Aug-2004
C;Accession: T26334
R;McMurray, A.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z20201
A;Accession: T26334
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-422 <WIL>
A;Cross-references: UNIPROT:Q94365; EMBL:Z81140; PIDN:CAB03485.1; GSPDB:GN00028; CESP:W1
A;Experimental source: clone W10G6
C;Genetics:
A;Gene: CESP:W10G6.2
A;Map position: X
A;Introns: 14/3; 60/2; 88/2; 135/3; 179/3; 217/2; 290/3; 393/1
C;Superfamily: protein kinase homology

  Query Match             12.9%;  Score 71.5;  DB 2;  Length 422;
  Best Local Similarity   27.6%;  Pred. No. 13;
  Matches   27;  Conservative   16;  Mismatches   34;  Indels   21;  Gaps    5;

Qy          12 VRPKPLLLK-----LLKSVG-------AQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIV 59
               ::|: |||       :|  |         | | |       ||   |: |: ||:
Db         219 LKPENLLLDDKGYLVLTDFGLCKEDMQGSKTTSTFCGTPEYLAPEIILKKPYDKTVDW-- 276

Qy          60 YCSNDLLGD-LFGVPSFSVKEHRKIYTMIYRNLVVVNQ 96
               :|   :| : :||:| |  |:| ::|  |      :||
Db         277 WCLGSVLYEMIFGLPPFYSKDHNEMYDKI------INQ 308


RESULT 12
D85069
hypothetical protein AT4g05520 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: D85069
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: D85069
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-514 <STO>
A;Cross-references: UNIPROT:Q9S9W1; GB:NC_001268; NID:g7267312; PIDN:CAB81094.1; GSPDB:G
C;Genetics:
A;Gene: AT4g05520
A;Map position: 4

  Query Match             12.9%;  Score 71.5;  DB 2;  Length 514;
  Best Local Similarity   29.7%;  Pred. No. 16;
  Matches   27;  Conservative   13;  Mismatches   26;  Indels   25;  Gaps    4;

Qy          15 KPLLLKLLKSVGA-----QKDTYTMKEVLYYLGQY-----------IMTKRLYDEKQQHI 58
               :|| |||::  ||       |   | : |  |:| :            : | |::::|
Db         384 QPLFLKLMRVYGALMWSLGKVLNTPEVVRVYIGSFNDKPINEVAVGPIGKELFEKEQ--- 440

Qy          59 VYCSNDLLGDLFGVPSFSVKEHRKIYTMIYR 89
                     |||| ||  ||  :    |||   : |
```

```
Db         441 ----NDLLADLMDVPKKAC--DRKINEFVKR 465


RESULT 13
XUBYMC
methylated-DNA-[protein]-cysteine S-methyltransferase (EC 2.1.1.63) [similarity] - yeast
N;Alternate names: DNA repair methyltransferase; O(4)-methylthymine-DNA alkyltransferase
ltransferase; protein D1204; protein YDL200c
C;Species: Saccharomyces cerevisiae
C;Date: 31-Mar-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S29370; S16713; S58777; S67759; S67755; S72060
R;Xiao, W.; Samson, L.
Nucleic Acids Res. 20, 3599-3606, 1992
A;Title: The Saccharomyces cerevisiae MGT1 DNA repair methyltransferase gene: its promot
A;Reference number: S29370; MUID:92350658; PMID:1641326
A;Accession: S29370
A;Molecule type: DNA
A;Residues: 1-206 <XIA>
A;Cross-references: UNIPROT:P26188; EMBL:M94227; NID:g171948; PIDN:AAA34780.1; PID:g1719
A;Experimental source: strain DBY747
R;Xiao, W.; Derfler, B.; Chen, J.; Samson, L.
EMBO J. 10, 2179-2186, 1991
A;Title: Primary sequence and biological functions of a Saccharomyces cerevisiae O(6)-me
A;Reference number: S16713; MUID:91293093; PMID:2065659
A;Accession: S16713
A;Molecule type: DNA
A;Residues: 13-206 <XI2>
A;Cross-references: EMBL:X60368
A;Experimental source: strain DBY747
R;Verhasselt, P.; Voet, M.; Volckaert, G.
submitted to the EMBL Data Library, December 1994
A;Reference number: S58777
A;Accession: S58777
A;Molecule type: DNA
A;Residues: 19-152 <VER>
A;Cross-references: EMBL:X83276
R;Schmidt, E.R.; Bahr, A.; Kraemer, C.; Hankeln, T.; Moeller-Rieker, S.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67756
A;Accession: S67759
A;Molecule type: DNA
A;Residues: 1-206 <SCH>
A;Cross-references: EMBL:Z74248; NID:g1431329; PIDN:CAA98778.1; PID:g1431330; GSPDB:GN00
A;Experimental source: strain S288C
R;Volckaert, G.; Verhasselt, P.; Voet, M.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67735
A;Accession: S67755
A;Molecule type: DNA
A;Residues: 1-152 <VOL>
A;Cross-references: EMBL:Z74248; GSPDB:GN00004; MIPS:YDL200c
A;Experimental source: strain S288C
R;Verhasselt, P.; Voet, M.; Mathys, J.; Volckaert, G.
Yeast 12, 1065-1070, 1996
A;Title: The sequence of 23 kb surrounding the SNF3 locus on the left arm of yeast chrom
ing putative genes for ribosomal protein L35 and a sugar transport protein.
A;Reference number: S72060; MUID:97051595; PMID:8896272
A;Accession: S72060
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 19-152 <VEW>
A;Cross-references: EMBL:X83276
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1994
C;Genetics:
A;Gene: SGD:MGT1; MIPS:YDL200c
A;Cross-references: MIPS:YDL200c; SGD:S0002359
A;Map position: 4L
C;Function:
A;Description: DNA repair; methyltransferase; removes methyl groups from O(6)-methylguan
C;Superfamily: methylated-DNA-protein-cysteine S-methyltransferase; methylated-DNA-prote
C;Keywords: DNA repair; methylated amino acid; methyltransferase
F;116-196/Domain: methylated-DNA-protein-cysteine S-methyltransferase homology <MGT>
F;169/Binding site: methyl (Cys) (covalent) #status predicted
```

```
  Query Match             12.8%;  Score 71;  DB 1;  Length 206;
  Best Local Similarity   41.0%;  Pred. No. 6.5;
  Matches   25;  Conservative   10;  Mismatches   16;  Indels   10;  Gaps    4;

Qy         33 TMKEVLYYLGQYIMTK-----RLYDEKQQHIVYCS--NDLLGDLFGVPSFSVKEHRKIYT 85
              ||||:|||   :| |:       :: || |::|: |  || |  |  |  | :|:| |  |
Db         18 TMKELLYY--TFIETEVTGAFLVFREKTQNLVFASLGNDKLFLLGKVEGF-LKKHEKQDT 74

Qy         86 M 86
              |
Db         75 M 75


RESULT 14
I45557
eyeless, long form - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 16-Aug-2004
C;Accession: I45557
R;Quiring, R.; Walldorf, U.; Kloter, U.; Gehring, W.J.
Science 265, 785-789, 1994
A;Title: Homology of the eyeless gene of Drosophila to the Small eye gene in mice and An
A;Reference number: A54584; MUID:94323757; PMID:7914031
A;Accession: I45557
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-838 <RES>
A;Cross-references: EMBL:X79493; NID:g641809; PIDN:CAA56038.1; PID:g641810
C;Genetics:
A;Gene: FlyBase:ey
A;Cross-references: FlyBase:FBgn0005558
A;Introns: 37/1; 92/2; 152/3; 371/1; 429/1; 521/1; 639/2
C;Superfamily: homeobox homology; paired box homology
C;Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulati
F;37-161/Domain: paired box homology <PBH>
F;412-468/Domain: homeobox homology <HOX>

  Query Match             12.7%;  Score 70.5;  DB 2;  Length 838;
  Best Local Similarity   26.0%;  Pred. No. 36;
  Matches   26;  Conservative   14;  Mismatches   33;  Indels   27;  Gaps    5;

Qy         12 VRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQY------IMTKRLYDEKQQHIVYCSNDL 65
              :||       :::|  |      ||:  : ||      |    : |  |  | |:||
Db         99 IRP--------RAIGGSKPRVATAEVVSKISQYKRECPSIFAWEIRDRLLQENV-CTND- 148

Qy         66 LGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTS 105
                 :|| |          : |||    :|:|: ||:|
Db        149 -----NIPSVS------SINRVLRNLAAQKEQQSTGSGSS 177


RESULT 15
B84938
flagellar motor switch protein fliG [imported] - Buchnera sp. (strain APS)
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 24-Aug-2001
C;Accession: B84938
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A
A;Reference number: A84930; MUID:20445173; PMID:10993077
A;Accession: B84938
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-331 <STO>
A;Cross-references: GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
C;Genetics:
A;Gene: fliG; BU074
C;Superfamily: flagellar switch protein fliG

  Query Match             12.5%;  Score 69.5;  DB 2;  Length 331;
  Best Local Similarity   26.4%;  Pred. No. 16;
  Matches   23;  Conservative   16;  Mismatches   31;  Indels   17;  Gaps    2;

Qy         15 KPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVYCSNDLLGDLFGVPS 74
              | |:  | |::| :| |  :|| |       |  | |   | : : :  :
Db         75 KYLIKMLTKALGEKKGTSLLKEALEIRNARICIKALNYMKAKQVAFLLD---------- 123

Qy         75 FSVKEHRKIYTMIYRNLVVVNQQESSD 101
                 ||| :| | |   |: :|: :|::
Db        124 ---KEHPQIITTI---LICLNKNQSAE 144


Search completed: January 27, 2005, 18:15:10
Job time : 20.8 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:59:36 ; Search time 69.4 Seconds
(without alignments)
567.443 Million cell updates/sec

Title: US-10-822-254-8
Perfect score: 554
Sequence: 1 SQIPASEQETLVRPKPLLLK.....NLVVVNQQESSDSGTSVSEN 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	550	99.3	491	9	US-09-888-077-1	Sequence 1, Appli
2	550	99.3	491	9	US-09-956-425-8	Sequence 8, Appli
3	550	99.3	491	10	US-09-029-327-2	Sequence 2, Appli
4	550	99.3	491	11	US-09-966-724-2	Sequence 2, Appli
5	550	99.3	491	15	US-10-422-536-137	Sequence 137, App
6	550	99.3	491	15	US-10-232-951-35	Sequence 35, Appl
7	550	99.3	491	17	US-10-685-838-1	Sequence 1, Appli
8	550	99.3	491	17	US-10-724-225-2	Sequence 2, Appli
9	550	99.3	491	17	US-10-489-802-8	Sequence 8, Appli
10	550	99.3	491	17	US-10-723-860-2236	Sequence 2236, Ap
11	533.5	96.3	216	13	US-10-057-510-4	Sequence 4, Appli
12	524.5	94.7	522	15	US-10-287-226-380	Sequence 380, App
13	524.5	94.7	522	15	US-10-287-226-382	Sequence 382, App
14	490.5	88.5	489	9	US-09-956-425-6	Sequence 6, Appli
15	490.5	88.5	489	11	US-09-966-724-4	Sequence 4, Appli
16	490.5	88.5	489	17	US-10-489-802-6	Sequence 6, Appli
17	483	87.2	95	17	US-10-685-838-2	Sequence 2, Appli
18	474	85.6	95	17	US-10-685-838-4	Sequence 4, Appli
19	470	84.8	92	17	US-10-685-838-3	Sequence 3, Appli
20	311	56.1	59	14	US-10-211-088-143	Sequence 143, App
21	76	13.7	472	14	US-10-369-493-16585	Sequence 16585, A
22	76	13.7	473	15	US-10-282-122A-45311	Sequence 45311, A
23	76	13.7	967	15	US-10-282-122A-59020	Sequence 59020, A
24	72.5	13.1	578	16	US-10-437-963-174237	Sequence 174237,
25	72	13.0	969	15	US-10-335-977-7409	Sequence 7409, Ap
26	72	13.0	972	15	US-10-335-977-7410	Sequence 7410, Ap
27	71.5	12.9	328	17	US-10-425-115-191466	Sequence 191466,
28	71.5	12.9	422	14	US-10-369-493-7027	Sequence 7027, Ap
29	70	12.6	383	15	US-10-424-599-282528	Sequence 282528,
30	70	12.6	613	16	US-10-437-963-113326	Sequence 113326,
31	69.5	12.5	277	15	US-10-282-122A-75363	Sequence 75363, A
32	69.5	12.5	291	15	US-10-425-114-59572	Sequence 59572, A
33	69.5	12.5	291	17	US-10-425-115-191465	Sequence 191465,
34	69.5	12.5	438	10	US-09-769-787-48	Sequence 48, Appl
35	68	12.3	650	15	US-10-403-571-96	Sequence 96, Appl
36	68	12.3	1031	16	US-10-437-963-189155	Sequence 189155,
37	67.5	12.2	92	17	US-10-425-115-264585	Sequence 264585,
38	67.5	12.2	225	15	US-10-282-122A-52429	Sequence 52429, A
39	67.5	12.2	498	14	US-10-369-493-20438	Sequence 20438, A
40	67.5	12.2	709	15	US-10-282-122A-63455	Sequence 63455, A
41	67	12.1	184	14	US-10-097-111-316	Sequence 316, App
42	67	12.1	705	15	US-10-425-114-57081	Sequence 57081, A
43	67	12.1	705	17	US-10-425-115-365082	Sequence 365082,
44	66.5	12.0	187	17	US-10-425-115-227933	Sequence 227933,
45	66.5	12.0	315	15	US-10-282-122A-55168	Sequence 55168, A

ALIGNMENTS

RESULT 1
US-09-888-077-1
; Sequence 1, Application US/09888077
; Patent No. US20020031818A1
; GENERAL INFORMATION:
; APPLICANT: Ronai, Ze'ev
; APPLICANT: Fuchs, Serge
; TITLE OF INVENTION: Modification of Mdm2 Activity
; FILE REFERENCE: 2420/1H195-US1
; CURRENT APPLICATION NUMBER: US/09/888,077
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,343
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-888-077-1

Query Match 99.3%; Score 550; DB 9; Length 491;
Best Local Similarity 99.1%; Pred. No. 1.4e-56;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              |||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125
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RESULT 2
US-09-956-425-8

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; Sequence 8, Application US/09956425
; Patent No. US20020045192A1
; GENERAL INFORMATION:
;  APPLICANT: Kriwacki, Richard
;  APPLICANT:  Bothner, Brian
;  APPLICANT:  Lewis, William
;  TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and Method of Use Thereof
;  FILE REFERENCE: 1340/1/035
;  CURRENT APPLICATION NUMBER: US/09/956,425
;  CURRENT FILING DATE:  2001-09-19
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-956-425-8

  Query Match             99.3%;  Score 550;  DB 9;  Length 491;
  Best Local Similarity   99.1%;  Pred. No. 1.4e-56;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 3
US-09-029-327-2
; Sequence 2, Application US/09029327
; Publication No. US20030060432A1
;  GENERAL INFORMATION:
;    APPLICANT:  TOCQUE, Bruno
;    APPLICANT:  WASYLYK, Bohdan
;    APPLICANT:  DUBS-POTERSZMAN,
;    APPLICANT:  Marie-Christine
;    TITLE OF INVENTION:  ANTAGONISTS OF THE ONCOGENIC ACTIVITY OF
;    TITLE OF INVENTION:  THE PROTEIN MDM2, AND USE THEREOF IN THE TREATMENT OF
;    TITLE OF INVENTION:  CANCERS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rhone-Poulenc Rorer Inc.
;      STREET:  500 Arcola Road, Mailstop 3C43
;      CITY:  Collegeville
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19426
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/029,327
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR 96/01340
;      FILING DATE:  02-SEP-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO FR95/10331
;      FILING DATE:  04-SEP-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fehlner Esq., Paul F.
;      REGISTRATION NUMBER:  35,135
;      REFERENCE/DOCKET NUMBER:  ST95050-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (610) 454-3839
;      TELEFAX:  (610) 454-3808
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-029-327-2

  Query Match             99.3%;  Score 550;  DB 10;  Length 491;
  Best Local Similarity   99.1%;  Pred. No. 1.4e-56;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 4
US-09-966-724-2
; Sequence 2, Application US/09966724
; Publication No. US20040170971A1
;  GENERAL INFORMATION:
;       APPLICANT: THE JOHNS HOPKINS UNIVERSITY
;                  720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA
;       TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
;                           HUMAN TUMORS
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
;            STREET: 1001 G ST., N.W.
;            CITY: WASHINGTON
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20001-4597
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/966,724
;            FILING DATE: 01-Oct-2001
;            CLASSIFICATION: 435
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/044,619
;            FILING DATE: 2001-10-01
;            APPLICATION NUMBER: US 07/867.840
;            FILING DATE: 07-APR-1992
;       ATTORNEY/AGENT INFORMATION:
;            NAME: KAGAN, SARAH A.
;            REGISTRATION NUMBER: 32,141
;            REFERENCE/DOCKET NUMBER: 01107.40148
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-508-9100
;            TELEFAX: 202-508-9299
;            TELEX: 197430 BBMB UT
;  INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 491 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-966-724-2

  Query Match             99.3%;  Score 550;  DB 11;  Length 491;
  Best Local Similarity   99.1%;  Pred. No. 1.4e-56;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 5
US-10-422-536-137
; Sequence 137, Application US/10422536
; Publication No. US20040014100A1
; GENERAL INFORMATION:
;  APPLICANT: Kinsella, Todd
;  APPLICANT:  Lorens, James
;  APPLICANT:  Pray, Todd
;  APPLICANT:  Bennett, Mark
;  TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR INHIBITING
;  TITLE OF INVENTION:  PROTEIN-PROTEIN INTERACTION
;  FILE REFERENCE: A-71433-1/AMP/CYO
;  CURRENT APPLICATION NUMBER: US/10/422,536
;  CURRENT FILING DATE:  2003-04-23
;  PRIOR APPLICATION NUMBER: US 60/187,130
;  PRIOR FILING DATE: 2000-03-06
;  PRIOR APPLICATION NUMBER: US 09/800,770
;  PRIOR FILING DATE: 2001-03-06
;  PRIOR APPLICATION NUMBER: US 10/232,758
;  PRIOR FILING DATE: 2002-08-30
;  NUMBER OF SEQ ID NOS: 168
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 137
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-422-536-137

  Query Match             99.3%;  Score 550;  DB 15;  Length 491;
  Best Local Similarity   99.1%;  Pred. No. 1.4e-56;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 6
US-10-232-951-35
; Sequence 35, Application US/10232951
; Publication No. US20040043386A1
; GENERAL INFORMATION:
;  APPLICANT: Pray, Todd
;  APPLICANT:  Wong, Brian
;  APPLICANT:  Bennett, Mark
;  APPLICANT:  Parlati, Francesco
;  APPLICANT:  Rigel Pharmaceuticals, Incorporated
;  TITLE OF INVENTION: Methods and Compositions for Functional Ubiquitin
;  TITLE OF INVENTION:  Assays
;  FILE REFERENCE: 021044-006800US
;  CURRENT APPLICATION NUMBER: US/10/232,951
;  CURRENT FILING DATE:  2002-08-30
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: E3 ubiquitin ligating agent mouse double minute 2
;   OTHER INFORMATION: (mdm2) homolog full length protein isoform, mouse
;   OTHER INFORMATION: p53-binding protein (MDM2) homolog, transcript
;   OTHER INFORMATION: variant MDM2, transformed 3T3 cell double minute 2,
;   OTHER INFORMATION: Mdm2 cDNA
US-10-232-951-35

  Query Match             99.3%;  Score 550;  DB 15;  Length 491;
  Best Local Similarity   99.1%;  Pred. No. 1.4e-56;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 7
US-10-685-838-1
; Sequence 1, Application US/10685838
; Publication No. US20040197893A1
; GENERAL INFORMATION:
;  APPLICANT: SHUBERT, CARSTEN
;  APPLICANT:  GRASBERGER, BRUCE
;  APPLICANT:  MAGUIRE, DIANE
;  APPLICANT:  DECKMAN, INGRID
;  APPLICANT:  SPURLINO, JOHN
;  TITLE OF INVENTION: HDM2-INHIBITOR COMPLEXES AND USES THEREOF
;  FILE REFERENCE: PRD-2137-USANP
;  CURRENT APPLICATION NUMBER: US/10/685,838
;  CURRENT FILING DATE:  2003-10-15
;  PRIOR APPLICATION NUMBER: 60/418,350
;  PRIOR FILING DATE: 2002-10-16
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-685-838-1

  Query Match             99.3%;  Score 550;  DB 17;  Length 491;
  Best Local Similarity   99.1%;  Pred. No. 1.4e-56;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 8
US-10-724-225-2
; Sequence 2, Application US/10724225
; Publication No. US20040209834A1
;   GENERAL INFORMATION:
;        APPLICANT: TOCQUE, Bruno
;                   WASYLYK, Bohdan
;                   DUBS-POTERSZMAN,
;                   Marie-Christine
;        TITLE OF INVENTION: ANTAGONISTS OF THE ONCOGENIC ACTIVITY OF
;                            THE PROTEIN MDM2, AND USE THEREOF IN THE TREATMENT OF
;                            CANCERS
;        NUMBER OF SEQUENCES: 4
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Rhone-Poulenc Rorer Inc.
;             STREET: 500 Arcola Road, Mailstop 3C43
;             CITY: Collegeville
```

; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/724,225
; FILING DATE: 01-Dec-2003
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/029,327
; FILING DATE: <Unknown>
; APPLICATION NUMBER: FR 96/01340
; FILING DATE: 02-SEP-1996
; APPLICATION NUMBER: WO FR95/10331
; FILING DATE: 04-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fehlner Esq., Paul F.
; REGISTRATION NUMBER: 35,135
; REFERENCE/DOCKET NUMBER: ST95050-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-724-225-2

Query Match 99.3%; Score 550; DB 17; Length 491;
Best Local Similarity 99.1%; Pred. No. 1.4e-56;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125

RESULT 9
US-10-489-802-8
; Sequence 8, Application US/10489802
; Publication No. US20040248198A1
; GENERAL INFORMATION:
; APPLICANT: St. Jude Children's Research Hospital, Inc.
; APPLICANT: Kriwacki, Richard
; APPLICANT: Bothner, Brian
; APPLICANT: Lewis, William
; TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and
; TITLE OF INVENTION: Method of Use Thereof
; FILE REFERENCE: 44158/243642
; CURRENT APPLICATION NUMBER: US/10/489,802
; CURRENT FILING DATE: 2004-03-16
; PRIOR APPLICATION NUMBER: US 09/956,425
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-489-802-8

Query Match 99.3%; Score 550; DB 17; Length 491;
Best Local Similarity 99.1%; Pred. No. 1.4e-56;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125

RESULT 10
US-10-723-860-2236
; Sequence 2236, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2236
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-2236

Query Match 99.3%; Score 550; DB 17; Length 491;
Best Local Similarity 99.1%; Pred. No. 1.4e-56;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125

RESULT 11
US-10-057-510-4
; Sequence 4, Application US/10057510
; Publication No. US20020098580A1
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Yang, Meijia
; APPLICANT: Schulz, Vincent
; APPLICANT: CuraGen Corporation
; TITLE OF INVENTION: MDM INTERACTING PROTEIN AND METHODS OF USE THEREOF
; FILE REFERENCE: 15966-524 MDM US
; CURRENT APPLICATION NUMBER: US/10/057,510
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: USSN 09/510,252
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: USSN 60/121,192
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: USSN 60/122,643
; PRIOR FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens

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US-10-057-510-4

  Query Match             96.3%;  Score 533.5;  DB 13;  Length 216;
  Best Local Similarity   98.2%;  Pred. No. 4.4e-55;
  Matches  107;  Conservative    1;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||:|| ||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYL-QYIMTKRLYDEKQQHIVY 75

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 124


RESULT 12
US-10-287-226-380
; Sequence 380, Application US/10287226
; Publication No. US20040086875A1
; GENERAL INFORMATION:
;  APPLICANT: Agee, Michele L.,
;  APPLICANT:  Alsobrook, John P.,
;  APPLICANT:  Berghs, Constance,
;  APPLICANT:  Boldog, Ference,
;  APPLICANT:  Burgess, Catherine E.,
;  APPLICANT:  Chant, John S.,
;  APPLICANT:  Chaudhuri, Amitabha,
;  APPLICANT:  DiPippo, Vincent A.,
;  APPLICANT:  Edinger, Shlomit R.,
;  APPLICANT:  Eisen, Andrew,
;  APPLICANT:  Ellerman, Karen,
;  APPLICANT:  Gangolli, Esha A.,
;  APPLICANT:  Gorman, Linda,
;  APPLICANT:  Gerlach, Valerie,
;  APPLICANT:  Ji, Weizhen,
;  APPLICANT:  Kekuda, Ramesh,
;  APPLICANT:  Khramtsov, Nikolai,
;  APPLICANT:  Li, Li,
;  APPLICANT:  Malyankar, Uriel M.,
;  APPLICANT:  MacDougall, John R.,
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Miller, Charles E.,
;  APPLICANT:  Millet, Isabelle,
;  APPLICANT:  Ooi, Chean Eng,
;  APPLICANT:  Ort, Tatiana,
;  APPLICANT:  Padigaru, Muralidhara,
;  APPLICANT:  Patturajan, Meera,
;  APPLICANT:  Rastelli, Luca,
;  APPLICANT:  Rieger, Daniel K.,
;  APPLICANT:  Rothenberg, Mark E.,
;  APPLICANT:  Shenoy, Suresh G.,
;  APPLICANT:  Spaderna, Steven K.,
;  APPLICANT:  Spytek, Kimberley A.,
;  APPLICANT:  Taupier, Jr., Raymond J.,
;  APPLICANT:  Vernet, Corine A.M.,
;  APPLICANT:  Zerhusen, Bryan D.,
;  APPLICANT:  Zhong, Mei
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-480C
;  CURRENT APPLICATION NUMBER: US/10/287,226
;  CURRENT FILING DATE:  2002-11-04
;  PRIOR APPLICATION NUMBER: 60/334,421
;  PRIOR FILING DATE: 2001-11-30
;  PRIOR APPLICATION NUMBER: 60/354,392
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: 60/360,148
;  PRIOR FILING DATE: 2002-02-27
;  PRIOR APPLICATION NUMBER: 60/364,000
;  PRIOR FILING DATE: 2002-03-13
;  PRIOR APPLICATION NUMBER: 60/404,821
;  PRIOR FILING DATE: 2002-08-20
;  PRIOR APPLICATION NUMBER: 60/334,526
;  PRIOR FILING DATE: 2001-11-30
;  PRIOR APPLICATION NUMBER: 60/354,409
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: 60/364,227
;  PRIOR FILING DATE: 2002-03-13
;  PRIOR APPLICATION NUMBER: 60/334,027
;  PRIOR FILING DATE: 2001-11-28
;  PRIOR APPLICATION NUMBER: 60/331,641
;  PRIOR FILING DATE: 2001-11-20
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 673
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 380
;   LENGTH: 522
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-287-226-380

  Query Match             94.7%;  Score 524.5;  DB 15;  Length 522;
  Best Local Similarity   77.1%;  Pred. No. 1.7e-53;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels   31;  Gaps    1;

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Qy         37 -------VLYYLGQYIMTKRLYDEKQQHIVYCSNDLLGDLFGVPSFSVKEHRKIYTMIYR 89
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Qy         90 NLVVVNQQESSDSGTSVSEN 109
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Db        137 NLVVVNQQESSDSGTSVSEN 156


RESULT 13
US-10-287-226-382
; Sequence 382, Application US/10287226
; Publication No. US20040086875A1
; GENERAL INFORMATION:
;  APPLICANT: Agee, Michele L.,
;  APPLICANT:  Alsobrook, John P.,
;  APPLICANT:  Berghs, Constance,
;  APPLICANT:  Boldog, Ference,
;  APPLICANT:  Burgess, Catherine E.,
;  APPLICANT:  Chant, John S.,
;  APPLICANT:  Chaudhuri, Amitabha,
;  APPLICANT:  DiPippo, Vincent A.,
;  APPLICANT:  Edinger, Shlomit R.,
;  APPLICANT:  Eisen, Andrew,
;  APPLICANT:  Ellerman, Karen,
;  APPLICANT:  Gangolli, Esha A.,
;  APPLICANT:  Gorman, Linda,
;  APPLICANT:  Gerlach, Valerie,
;  APPLICANT:  Ji, Weizhen,
;  APPLICANT:  Kekuda, Ramesh,
;  APPLICANT:  Khramtsov, Nikolai,
;  APPLICANT:  Li, Li,
;  APPLICANT:  Malyankar, Uriel M.,
;  APPLICANT:  MacDougall, John R.,
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Miller, Charles E.,
;  APPLICANT:  Millet, Isabelle,
;  APPLICANT:  Ooi, Chean Eng,
;  APPLICANT:  Ort, Tatiana,
;  APPLICANT:  Padigaru, Muralidhara,
;  APPLICANT:  Patturajan, Meera,
;  APPLICANT:  Rastelli, Luca,
;  APPLICANT:  Rieger, Daniel K.,
;  APPLICANT:  Rothenberg, Mark E.,
;  APPLICANT:  Shenoy, Suresh G.,
;  APPLICANT:  Spaderna, Steven K.,
;  APPLICANT:  Spytek, Kimberley A.,
;  APPLICANT:  Taupier, Jr., Raymond J.,
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;  APPLICANT:  Vernet, Corine A.M.,
;  APPLICANT:  Zerhusen, Bryan D.,
;  APPLICANT:  Zhong, Mei
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-480C
;  CURRENT APPLICATION NUMBER: US/10/287,226
;  CURRENT FILING DATE:  2002-11-04
;  PRIOR APPLICATION NUMBER: 60/334,421
;  PRIOR FILING DATE: 2001-11-30
;  PRIOR APPLICATION NUMBER: 60/354,392
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: 60/360,148
;  PRIOR FILING DATE: 2002-02-27
;  PRIOR APPLICATION NUMBER: 60/364,000
;  PRIOR FILING DATE: 2002-03-13
;  PRIOR APPLICATION NUMBER: 60/404,821
;  PRIOR FILING DATE: 2002-08-20
;  PRIOR APPLICATION NUMBER: 60/334,526
;  PRIOR FILING DATE: 2001-11-30
;  PRIOR APPLICATION NUMBER: 60/354,409
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: 60/364,227
;  PRIOR FILING DATE: 2002-03-13
;  PRIOR APPLICATION NUMBER: 60/334,027
;  PRIOR FILING DATE: 2001-11-28
;  PRIOR APPLICATION NUMBER: 60/331,641
;  PRIOR FILING DATE: 2001-11-20
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 673
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 382
;   LENGTH: 522
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-287-226-382

  Query Match             94.7%;  Score 524.5;  DB 15;  Length 522;
  Best Local Similarity   77.1%;  Pred. No. 1.7e-53;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels   31;  Gaps    1;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKE---------------------- 36
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Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKERWSFTMLPRLVWNSWAQGICLPRP 76

Qy         37 -------VLYYLGQYIMTKRLYDEKQQHIVYCSNDLLGDLFGVPSFSVKEHRKIYTMIYR 89
                   ||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 PKVLDLQVLFYLGQYIMTKRLYDEKQQHIVYCSNDLLGDLFGVPSFSVKEHRKIYTMIYR 136

Qy         90 NLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||
Db        137 NLVVVNQQESSDSGTSVSEN 156


RESULT 14
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; Sequence 6, Application US/09956425
; Patent No. US20020045192A1
; GENERAL INFORMATION:
;  APPLICANT: Kriwacki, Richard
;  APPLICANT:  Bothner, Brian
;  APPLICANT:  Lewis, William
;  TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and Method of Use Thereof
;  FILE REFERENCE: 1340/1/035
;  CURRENT APPLICATION NUMBER: US/09/956,425
;  CURRENT FILING DATE:  2001-09-19
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 489
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-956-425-6

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  Best Local Similarity   87.2%;  Pred. No. 1.7e-49;
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Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
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Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQNDTYTMKEIIFYIGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
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RESULT 15
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; Sequence 4, Application US/09966724
; Publication No. US20040170971A1
;  GENERAL INFORMATION:
;       APPLICANT: THE JOHNS HOPKINS UNIVERSITY
;                  720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA
;       TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
;                           HUMAN TUMORS
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
;            STREET: 1001 G ST., N.W.
;            CITY: WASHINGTON
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20001-4597
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/966,724
;            FILING DATE: 01-Oct-2001
;            CLASSIFICATION: 435
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/044,619
;            FILING DATE: 2001-10-01
;            APPLICATION NUMBER: US 07/867.840
;            FILING DATE: 07-APR-1992
;       ATTORNEY/AGENT INFORMATION:
;            NAME: KAGAN, SARAH A.
;            REGISTRATION NUMBER: 32,141
;            REFERENCE/DOCKET NUMBER: 01107.40148
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-508-9100
;            TELEFAX: 202-508-9299
;            TELEX: 197430 BBMB UT
;   INFORMATION FOR SEQ ID NO: 4:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 489 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-966-724-4

  Query Match             88.5%;  Score 490.5;  DB 11;  Length 489;
  Best Local Similarity   87.2%;  Pred. No. 1.7e-49;
  Matches   95;  Conservative    8;  Mismatches    3;  Indels    3;  Gaps    1;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
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Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
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Db         77 CSNDLLGDVFGVPSFSVKEHRKIYAMIYRNLVAVSQQ---DSGTSLSES 122
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GenCore version 5.1.6

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325.615 Million cell updates/sec

Title: US-10-822-254-8
Perfect score: 554
Sequence: 1 SQIPASEQETLVRPKPLLLK.....NLVVVNQQESSDSGTSVSEN 109

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Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	550	99.3	491	1	US-07-903-103-2	Sequence 2, Appli
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4	550	99.3	491	1	US-08-283-911-2	Sequence 2, Appli
5	550	99.3	491	1	US-08-245-500A-3	Sequence 3, Appli
6	550	99.3	491	1	US-08-390-546-3	Sequence 3, Appli
7	550	99.3	491	1	US-08-390-479A-3	Sequence 3, Appli
8	550	99.3	491	1	US-08-557-393-3	Sequence 3, Appli
9	550	99.3	491	1	US-08-390-516C-3	Sequence 3, Appli
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19	490.5	88.5	489	1	US-08-245-500A-5	Sequence 5, Appli
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23	490.5	88.5	489	1	US-08-390-516C-5	Sequence 5, Appli
24	490.5	88.5	489	1	US-08-390-517A-5	Sequence 5, Appli
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30	72.5	13.1	244	4	US-09-543-681A-6675	Sequence 6675, Ap
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34	66.5	12.0	590	3	US-09-232-191-25	Sequence 25, Appl
35	66.5	12.0	590	3	US-09-232-200-75	Sequence 75, Appl
36	66.5	12.0	590	3	US-09-232-197-75	Sequence 75, Appl
37	66.5	12.0	590	3	US-09-232-201-75	Sequence 75, Appl
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41	64.5	11.6	107	3	US-09-187-859-35	Sequence 35, Appl
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45	64.5	11.6	107	4	US-09-535-852-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1
US-09-603-052-4
; Sequence 4, Application US/09603052
; Patent No. 6492116
; GENERAL INFORMATION:
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; TITLE OF INVENTION: Assay for identifying inhibitors of the interaction
; TITLE OF INVENTION: between proteins p53 and dm2
; FILE REFERENCE: MEWB26.001C1
; CURRENT APPLICATION NUMBER: US/09/603,052
; CURRENT FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: EP 95810576.9
; PRIOR FILING DATE: 1995-09-18
; PRIOR APPLICATION NUMBER: PCT/EP96/03957
; PRIOR FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-603-052-4

Query Match 99.3%; Score 550; DB 4; Length 188;
Best Local Similarity 99.1%; Pred. No. 4.7e-61;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
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Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125
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RESULT 2
US-07-903-103-2
; Sequence 2, Application US/07903103
; Patent No. 5411860
; GENERAL INFORMATION:
; APPLICANT: VOGELSTEIN, BERT
; APPLICANT: KINZLER, KENNETH
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G ST., N.W.

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;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001-4597
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/903,103
;      FILING DATE:  19920623
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/867.840
;      FILING DATE:  07-APR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.40148
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-903-103-2

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              ||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
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Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 3
US-08-044-619A-2
; Sequence 2, Application US/08044619A
; Patent No. 5420263
;  GENERAL INFORMATION:
;    APPLICANT:  THE JOHNS HOPKINS UNIVERSITY
;    APPLICANT:  720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G ST., N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001-4597
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/044,619A
;      FILING DATE:  07-APR-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/903,103
;      FILING DATE:  23-JUN-1992
;      APPLICATION NUMBER:  US 07/867.840
;      FILING DATE:  07-APR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.40148
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-044-619A-2

  Query Match             99.3%;  Score 550;  DB 1;  Length 491;
  Best Local Similarity   99.1%;  Pred. No. 1.7e-60;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 4
US-08-283-911-2
; Sequence 2, Application US/08283911
; Patent No. 5519118
;  GENERAL INFORMATION:
;    APPLICANT:  VOGELSTEIN, BERT
;    APPLICANT:  KINZLER, KENNETH
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G ST., N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001-4597
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/283,911
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/903,103
;      FILING DATE:  23-JUN-1992
;      APPLICATION NUMBER:  US 07/867.840
;      FILING DATE:  07-APR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.40148
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-283-911-2

  Query Match             99.3%;  Score 550;  DB 1;  Length 491;
  Best Local Similarity   99.1%;  Pred. No. 1.7e-60;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 5
US-08-245-500A-3
; Sequence 3, Application US/08245500A
; Patent No. 5550023
;  GENERAL INFORMATION:
;    APPLICANT:  BURRELL, MARILEE
;    APPLICANT:  HILL, DAVID E.
;    APPLICANT:  KINZLER, KENNETH W.
;    APPLICANT:  VOGELSTEIN, BERT
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/245,500A
;      FILING DATE:  07-APR-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.42798
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-245-500A-3

  Query Match             99.3%;  Score 550;  DB 1;  Length 491;
  Best Local Similarity   99.1%;  Pred. No. 1.7e-60;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 6
US-08-390-546-3
; Sequence 3, Application US/08390546
; Patent No. 5606044
;  GENERAL INFORMATION:
;    APPLICANT:  BURRELL, MARILEE
;    APPLICANT:  HILL, DAVID E.
;    APPLICANT:  KINZLER, KENNETH W.
;    APPLICANT:  VOGELSTEIN, BERT
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/390,546
;      FILING DATE:  07-APR-1993
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.42798
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-390-546-3

  Query Match             99.3%;  Score 550;  DB 1;  Length 491;
  Best Local Similarity   99.1%;  Pred. No. 1.7e-60;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 7
US-08-390-479A-3
; Sequence 3, Application US/08390479A
; Patent No. 5618921
;  GENERAL INFORMATION:
;    APPLICANT:  BURRELL, MARILEE
;    APPLICANT:  HILL, DAVID E.
;    APPLICANT:  KINZLER, KENNETH W.
;    APPLICANT:  VOGELSTEIN, BERT
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
```

; ADDRESSEE: BANNER & WITCOFF, LTD.
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,479A
; FILING DATE: 02-FEB-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.48992
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-390-479A-3

Query Match 99.3%; Score 550; DB 1; Length 491;
Best Local Similarity 99.1%; Pred. No. 1.7e-60;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125
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RESULT 8
US-08-557-393-3
; Sequence 3, Application US/08557393
; Patent No. 5702903
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,393
; FILING DATE: 13-NOV-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/245,500
; FILING DATE: 18-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-557-393-3

Query Match 99.3%; Score 550; DB 1; Length 491;
Best Local Similarity 99.1%; Pred. No. 1.7e-60;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125
```

RESULT 9
US-08-390-516C-3
; Sequence 3, Application US/08390516C
; Patent No. 5708136
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,516C
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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US-08-390-516C-3

  Query Match             99.3%;  Score 550;  DB 1;  Length 491;
  Best Local Similarity   99.1%;  Pred. No. 1.7e-60;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 10
US-08-390-517A-3
; Sequence 3, Application US/08390517A
; Patent No. 5736338
;  GENERAL INFORMATION:
;    APPLICANT:  BURRELL, MARILEE
;    APPLICANT:  HILL, DAVID E.
;    APPLICANT:  KINZLER, KENNETH W.
;    APPLICANT:  VOGELSTEIN, BERT
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/390,517A
;      FILING DATE:  07-APR-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.42798
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-390-517A-3

  Query Match             99.3%;  Score 550;  DB 1;  Length 491;
  Best Local Similarity   99.1%;  Pred. No. 1.7e-60;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 11
US-08-390-515A-3
; Sequence 3, Application US/08390515A
; Patent No. 5756455
;  GENERAL INFORMATION:
;    APPLICANT:  BURRELL, MARILEE
;    APPLICANT:  HILL, DAVID E.
;    APPLICANT:  KINZLER, KENNETH W.
;    APPLICANT:  VOGELSTEIN, BERT
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/390,515A
;      FILING DATE:  07-APR-1993
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.42798
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-390-515A-3

  Query Match             99.3%;  Score 550;  DB 1;  Length 491;
  Best Local Similarity   99.1%;  Pred. No. 1.7e-60;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 12
US-08-801-718-3
; Sequence 3, Application US/08801718
; Patent No. 5858976
;  GENERAL INFORMATION:
;    APPLICANT:  BURRELL, MARILEE
;    APPLICANT:  HILL, DAVID E.
;    APPLICANT:  KINZLER, KENNETH W.
;    APPLICANT:  VOGELSTEIN, BERT
;    TITLE OF INVENTION:  AMPLIFICATION OF HUMAN MDM2 GENE IN
;    TITLE OF INVENTION:  HUMAN TUMORS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER, BIRCH, MCKIE AND BECKETT
;      STREET:  1001 G STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;
```

```
;      COUNTRY:  USA
;      ZIP:  20001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/801,718
;      FILING DATE:  14-FEB-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/390,515
;      FILING DATE:  07-APR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAGAN, SARAH A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  01107.42798
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;      TELEX:  197430 BBMB UT
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-801-718-3

  Query Match             99.3%;  Score 550;  DB 2;  Length 491;
  Best Local Similarity   99.1%;  Pred. No. 1.7e-60;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 13
US-09-170-159A-3
; Sequence 3, Application US/09170159A
; Patent No. 6399755
;   GENERAL INFORMATION:
;       APPLICANT: BURRELL, MARILEE
;                  HILL, DAVID E.
;                  KINZLER, KENNETH W.
;                  VOGELSTEIN, BERT
;       TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
;                           HUMAN TUMORS
;       NUMBER OF SEQUENCES: 5
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
;            STREET: 1001 G STREET, N.W.
;            CITY: WASHINGTON
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20001
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/170,159A
;            FILING DATE: 13-Oct-1998
;            CLASSIFICATION: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: KAGAN, SARAH A.
;            REGISTRATION NUMBER: 32,141
;            REFERENCE/DOCKET NUMBER: 01107.42798
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-508-9100
;            TELEFAX: 202-508-9299
;            TELEX: 197430 BBMB UT
;   INFORMATION FOR SEQ ID NO: 3:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 491 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-170-159A-3

  Query Match             99.3%;  Score 550;  DB 3;  Length 491;
  Best Local Similarity   99.1%;  Pred. No. 1.7e-60;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 14
US-09-480-718-44
; Sequence 44, Application US/09480718
; Patent No. 6407062
; GENERAL INFORMATION:
;  APPLICANT: Sherr, Charles J
;  APPLICANT: Quelle, Dawn E
;  APPLICANT: Weber, Jason D.
;  APPLICANT: Roussel, Martine F.
;  APPLICANT: Frederique, Zindy
;  TITLE OF INVENTION: ARF-19, A NOVEL REGULATOR OF THE MAMMALIAN CELL CYCLE
;  FILE REFERENCE: 1340-1-023 CIP 1
;  CURRENT APPLICATION NUMBER: US/09/480,718
;  CURRENT FILING DATE: 2000-01-07
;  EARLIER APPLICATION NUMBER: 09/129,855
;  EARLIER FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-480-718-44

  Query Match             99.3%;  Score 550;  DB 4;  Length 491;
  Best Local Similarity   99.1%;  Pred. No. 1.7e-60;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
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Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 15
US-09-510-252-4
; Sequence 4, Application US/09510252
; Patent No. 6372490
; GENERAL INFORMATION:
;  APPLICANT: Nandabalan, Krishnan
;  APPLICANT:  Yang, Meijia
;  APPLICANT:  Schulz, Vincent
```

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;  APPLICANT:  CuraGen Corporation
;  TITLE OF INVENTION: MDM INTERACTING PROTEIN AND METHODS OF USE THEREOF
;  FILE REFERENCE: 15966-524 MDM US
;  CURRENT APPLICATION NUMBER: US/09/510,252
;  CURRENT FILING DATE:  2000-02-22
;  PRIOR APPLICATION NUMBER: USSN 60/121,192
;  PRIOR FILING DATE: 1999-02-23
;  PRIOR APPLICATION NUMBER: USSN 60/122,643
;  PRIOR FILING DATE: 1999-03-03
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 216
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-510-252-4

  Query Match             96.3%;  Score 533.5;  DB 3;  Length 216;
  Best Local Similarity   98.2%;  Pred. No. 6.7e-59;
  Matches  107;  Conservative    1;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||:|| ||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYL-QYIMTKRLYDEKQQHIVY 75

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 124


Search completed: January 27, 2005, 18:17:07
Job time : 23.2 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:51:46 ; Search time 84.6 Seconds
(without alignments)
741.322 Million cell updates/sec

Title: US-10-822-254-8
Perfect score: 554
Sequence: 1 SQIPASEQETLVRPKPLLLK.....NLVVVNQQESSDSGTSVSEN 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	550	99.3	166	2	Q8NDW2	Q8ndw2 homo sapien
2	550	99.3	195	2	Q96DS4	Q96ds4 homo sapien
3	550	99.3	243	2	Q8TE47	Q8te47 homo sapien
4	550	99.3	491	1	MDM2_HUMAN	Q00987 homo sapien
5	550	99.3	491	2	AAP35922	Aap35922 homo sapi
6	550	99.3	491	2	AAH67077	Aah67077 homo sapi
7	538	97.1	487	1	MDM2_CANFA	P56950 canis famil
8	538	97.1	487	2	Q9GMZ6	Q9gmz6 canis famil
9	538	97.1	491	1	MDM2_HORSE	P56951 equus cabal
10	535	96.6	491	2	Q7YRZ8	Q7yrz8 felis silve
11	500	90.3	436	2	Q8WYJ2	Q8wyj2 homo sapien
12	490.5	88.5	489	1	MDM2_MOUSE	P23804 mus musculu
13	490.5	88.5	489	2	Q91XK7	Q91xk7 m mus muscu
14	473	85.4	118	2	Q8WYJ3	Q8wyj3 homo sapien
15	468.5	84.6	466	1	MDM2_MESAU	Q60524 mesocricetu
16	412	74.4	325	2	Q9PVL2	Q9pvl2 gallus gall
17	404	72.9	173	2	Q8TE46	Q8te46 homo sapien
18	362	65.3	473	1	MDM2_XENLA	P56273 xenopus lae
19	362	65.3	473	2	Q6GMB5	Q6gmb5 xenopus lae
20	361	65.2	482	2	Q6P3Q9	Q6p3q9 xenopus tro
21	361	65.2	482	2	AAH63898	Aah63898 xenopus t
22	336	60.6	105	2	Q8NDW0	Q8ndw0 homo sapien
23	320	57.8	426	2	Q9GK41	Q9gk41 canis famil
24	289.5	52.3	445	1	MDM2_BRARE	O42354 brachydanio
25	289.5	52.3	445	2	AAM00198	Aam00198 brachydan
26	280.5	50.6	446	2	Q8WYJ1	Q8wyj1 homo sapien
27	279.5	50.5	489	1	MDM4_MOUSE	O35618 mus musculu
28	276.5	49.9	489	2	Q9CYG1	Q9cyg1 m mus muscu
29	271	48.9	491	2	Q7ZUW7	Q7zuw7 brachydanio
30	270	48.7	490	2	Q99L86	Q99l86 mus musculu
31	269	48.6	475	2	Q7ZYI3	Q7zyi3 xenopus lae
32	257.5	46.5	134	2	Q6PHL8	Q6phl8 xenopus lae
33	257.5	46.5	134	2	AAH56503	Aah56503 xenopus l
34	254	45.8	153	2	Q6MZR7	Q6mzr7 homo sapien
35	254	45.8	153	2	CAE45961	Cae45961 homo sapi
36	254	45.8	490	2	AAH67299	Aah67299 homo sapi
37	252	45.5	490	1	MDM4_HUMAN	O15151 homo sapien
38	220	39.7	69	2	Q86WA4	Q86wa4 homo sapien
39	213	38.4	66	2	Q96DS3	Q96ds3 homo sapien
40	210	37.9	70	2	Q86WA3	Q86wa3 homo sapien
41	196	35.4	95	2	Q96DS1	Q96ds1 homo sapien
42	179.5	32.4	70	2	Q8NDW1	Q8ndw1 homo sapien
43	177	31.9	159	2	Q96DS0	Q96ds0 homo sapien
44	176	31.8	60	2	Q96DS5	Q96ds5 homo sapien
45	176	31.8	130	2	Q9H4C3	Q9h4c3 homo sapien

ALIGNMENTS

RESULT 1
Q8NDW2
ID Q8NDW2 PRELIMINARY; PRT; 166 AA.
AC Q8NDW2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE P53-binding protein.
GN Name=MDM2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bartel F., Pinkert D., Kappler M., Bache M., Schmidt H., Taubert H.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ491698; CAD36959.1; -.
DR HSSP; Q9UMT8; 1YCR.
DR GO; GO:0005634; C:nucleus; IEA.
DR InterPro; IPR010984; MDM2.
DR InterPro; IPR003121; SWIB_MDM2.
DR Pfam; PF02201; SWIB; 1.
SQ SEQUENCE 166 AA; 18900 MW; FA6B5BA18E85040D CRC64;

Query Match 99.3%; Score 550; DB 2; Length 166;
Best Local Similarity 99.1%; Pred. No. 8.8e-51;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              |||||||||||||||||||||||||||||||||||||:|||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125
```

RESULT 2
Q96DS4
ID Q96DS4 PRELIMINARY; PRT; 195 AA.
AC Q96DS4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MDM2 variant FB26.
GN Name=MDM2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Rhabdomyosarcoma tumor;

```
RA   Bartel F., Taylor A.C., Taubert H., Harris L.C.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF385323; AAL13243.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB_MDM2.
DR   Pfam; PF02201; SWIB; 1.
SQ   SEQUENCE   195 AA;  22161 MW;  4987AE567DB12D5D CRC64;

  Query Match             99.3%;  Score 550;  DB 2;  Length 195;
  Best Local Similarity   99.1%;  Pred. No. 1.1e-50;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 3
Q8TE47
ID   Q8TE47      PRELIMINARY;      PRT;   243 AA.
AC   Q8TE47;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   MDM2 isoform KB9 protein.
GN   Name=MDM2 isoform KB9;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymphocytes;
RA   Bartel F., Pinkert D., Kappler M., Bache M., Schmidt H., Taubert H.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ430612; CAD23251.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR   GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   GO; GO:0016567; P:protein ubiquitination; IEA.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB_MDM2.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
SQ   SEQUENCE   243 AA;  27317 MW;  9EB5D0142CF185A2 CRC64;

  Query Match             99.3%;  Score 550;  DB 2;  Length 243;
  Best Local Similarity   99.1%;  Pred. No. 1.4e-50;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 4
MDM2_HUMAN
ID   MDM2_HUMAN     STANDARD;      PRT;   491 AA.
AC   Q00987; Q13226; Q13297; Q13298; Q13299; Q13300; Q13301; Q9UGI3;
AC   Q9UMT8;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein
DE   Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Hdm2).
GN   Name=MDM2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM MDM2).
RX   MEDLINE=92310576; PubMed=1614537;
RA   Oliner J.D., Kinzler K.W., Meltzer P.S., George D.L., Vogelstein B.;
RT   "Amplification of a gene encoding a p53-associated protein in human
RT   sarcomas.";
RL   Nature 358:80-83(1992).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS MDM2-A; -B; -C; -D AND -E).
RC   TISSUE=Ovarian carcinoma;
RX   MEDLINE=96313107; PubMed=8705862;
RA   Sigalas I., Calvert A.H., Anderson J.J., Neal D.E., Lunec J.;
RT   "Alternatively spliced mdm2 transcripts with loss of p53 binding
RT   domain sequences: transforming ability and frequent detection in human
RT   cancer.";
RL   Nat. Med. 2:912-917(1996).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM MDM2-ALPHA).
RX   MEDLINE=20065171; PubMed=10597303;
RA   Veldhoen N., Metcalfe S., Milner J.;
RT   "A novel exon within the mdm2 gene modulates translation initiation in
RT   vitro and disrupts the p53-binding domain of mdm2 protein.";
RL   Oncogene 18:7026-7033(1999).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM MDM2).
RA   Rieder M.J., Livingston R.J., Braun A.C., Montoya M.A., Chung M.-W.,
RA   Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA   Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RT   "NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department
RT   of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM MDM2).
RC   TISSUE=Muscle;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [6]
RP   SEQUENCE OF 6-491 FROM N.A. (ISOFORM MDM2-A1).
RA   Liang H., Atkins H., Abdel-Fattah R., Suaeyun R., Lunec J.;
RT   "Genomic organisation of the human MDM2 oncogene and relationship to
RT   its alternatively spliced mRNA's.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
RN   [7]
```

```
RP   SEQUENCE OF 1-24 FROM N.A.
RX   MEDLINE=95380270; PubMed=7651818;
RA   Zauberman A., Flusberg D., Haupt Y., Barak Y., Oren M.;
RT   "A functional p53-responsive intronic promoter is contained within the
RT   human mdm2 gene.";
RL   Nucleic Acids Res. 23:2584-2592(1995).
RN   [8]
RP   SEQUENCE OF 1-9 FROM N.A.
RX   MEDLINE=97413643; PubMed=9270029;
RA   Landers J.E., Cassel S.L., George D.L.;
RT   "Translational enhancement of mdm2 oncogene expression in human tumor
RT   cells containing a stabilized wild-type p53 protein.";
RL   Cancer Res. 57:3562-3568(1997).
RN   [9]
RP   SEQUENCE OF 301-481 FROM N.A.
RX   MEDLINE=20542019; PubMed=11087894;
RA   Taubert H., Kappler M., Meye A., Bartel F., Schlott T.,
RA   Lautenschlaeger C., Bache M., Schmidt H., Wuerl P.;
RT   "A MboII polymorphism in exon 11 of the human MDM2 gene occuring in
RT   normal blood donors and in soft tissue sarcoma patients: an indication
RT   for an increased cancer susceptibility?";
RL   Mutat. Res. 456:39-44(2000).
RN   [10]
RP   MUTAGENESIS OF CYS-464.
RX   MEDLINE=98111004; PubMed=9450543;
RA   Honda R., Tanaka H., Yasuda H.;
RT   "Oncoprotein MDM2 is a ubiquitin ligase E3 for tumor suppressor p53.";
RL   FEBS Lett. 420:25-27(1997).
RN   [11]
RP   MUTAGENESIS OF CYS-449.
RX   MEDLINE=20190101; PubMed=10723139;
RA   Honda R., Yasuda H.;
RT   "Activity of MDM2, a ubiquitin ligase, toward p53 or itself is
RT   dependent on the RING finger domain of the ligase.";
RL   Oncogene 19:1473-1476(2000).
RN   [12]
RP   MUTAGENESIS.
RX   MEDLINE=20187618; PubMed=10722742;
RA   Fang S., Jensen J.P., Ludwig R.L., Vousden K.H., Weissman A.M.;
RT   "Mdm2 is a RING finger-dependent ubiquitin protein ligase for itself
RT   and p53.";
RL   J. Biol. Chem. 275:8945-8951(2000).
RN   [13]
RP   MUTAGENESIS OF CYS-441 AND CYS-478.
RX   MEDLINE=20076498; PubMed=10608892;
RA   Sharp D.A., Kratowicz S.A., Sank M.J., George D.L.;
RT   "Stabilization of the MDM2 oncoprotein by interaction with the
RT   structurally related MDMX protein.";
RL   J. Biol. Chem. 274:38189-38196(1999).
RN   [14]
RP   NUCLEOLAR LOCALIZATION SIGNAL.
RX   MEDLINE=20173879; PubMed=10707090;
RA   Lohrum M.A.E., Ashcroft M., Kubbutat M.H.G., Vousden K.H.;
RT   "Identification of a cryptic nucleolar-localization signal in MDM2.";
RL   Nat. Cell Biol. 2:179-181(2000).
RN   [15]
RP   PHOSPHORYLATION BY ATM.
RX   MEDLINE=20079591; PubMed=10611322;
RA   Khosravi R., Maya R., Gottlieb T., Oren M., Shiloh Y., Shkedy D.;
RT   "Rapid ATM-dependent phosphorylation of MDM2 precedes p53 accumulation
RT   in response to DNA damage.";
RL   Proc. Natl. Acad. Sci. U.S.A. 96:14973-14977(1999).
RN   [16]
RP   X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 25-109 IN COMPLEX WITH P53.
RX   MEDLINE=97081050; PubMed=8875929;
RA   Kussie P.H., Gorina S., Marechal V., Elenbaas B., Moreau J.,
RA   Levine A.J., Pavletich N.P.;
RT   "Structure of the MDM2 oncoprotein bound to the p53 tumor suppressor
RT   transactivation domain.";
RL   Science 274:948-953(1996).
CC   -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC       apoptosis by binding its transcriptional activation domain.
CC       Functions as a ubiquitin ligase E3, in the presence of E1 and E2,
CC       toward p53 and itself. Permits the nuclear export of p53 and
CC       targets it for proteasome-mediated proteolysis.
CC   -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity.
CC   -!- SUBUNIT: Binds p53, p73, ARF(P14), ribosomal protein L5 and
CC       specifically to RNA. Can interact also with retinoblastoma protein
CC       (RB), E1A-associated protein EP300 and the E2F1 transcription
CC       factor.
CC   -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed
CC       predominantly in the nucleoplasm. Interaction with ARF(P14)
CC       results in the localization of both proteins to the nucleolus. The
CC       nucleolar localization signals in both ARF(P14) and MDM2 may be
CC       necessary to allow efficient nucleolar localization of both
CC       proteins.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=8;
CC       Name=Mdm2;
CC         IsoId=Q00987-1; Sequence=Displayed;
CC       Name=Mdm2-A;
CC         IsoId=Q00987-2; Sequence=VSP_003208;
CC       Name=Mdm2-A1;
CC         IsoId=Q00987-3; Sequence=VSP_003208, VSP_003214;
CC       Name=Mdm2-B;
CC         IsoId=Q00987-4; Sequence=VSP_003209;
CC       Name=Mdm2-C;
CC         IsoId=Q00987-5; Sequence=VSP_003211;
CC       Name=Mdm2-D;
CC         IsoId=Q00987-6; Sequence=VSP_003210;
CC       Name=Mdm2-E;
CC         IsoId=Q00987-7; Sequence=VSP_003212, VSP_003213;
CC       Name=Mdm2-alpha;
CC         IsoId=Q00987-8; Sequence=VSP_003207;
CC   -!- TISSUE SPECIFICITY: Ubiquitous. Isoforms MDM2-A, -B, -C, -D and -E
CC       are observed in a range of human cancers but absent in normal
CC       tissues.
CC   -!- INDUCTION: By DNA damage.
CC   -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its
CC       G1 arrest and apoptosis functions. It also binds p73 and E2F1.
CC       Region II contains most of a central acidic region required for
CC       interaction with ribosomal protein L5 and a putative C4-type zinc
CC       finger. The RING finger domain which coordinates two molecules of
CC       zinc interacts specifically with RNA whether or not zinc is
CC       present and mediates the hetero-oligomerization with MDM4. It is
CC       also essential for its ubiquitin ligase E3 activity toward p53 and
CC       itself.
CC   -!- PTM: Phosphorylated in response to ionizing radiation in an ATM-
CC       dependent manner.
CC   -!- DISEASE: Seems to be amplified in certain tumors (including soft
CC       tissue sarcomas, osteosarcomas and gliomas). A higher frequency of
CC       splice variants lacking p53 binding domain sequences was found in
CC       late-stage and high-grade ovarian and bladder carcinomas. Four of
CC       the splice variants show loss of p53 binding.
CC   -!- MISCELLANEOUS: MDM2 RING finger mutations that failed to

  Query Match           99.3%;  Score 550;  DB 1;  Length 491;
  Best Local Similarity  99.1%;  Pred. No. 3.1e-50;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 5
AAP35922
ID   AAP35922    PRELIMINARY;      PRT;   491 AA.
AC   AAP35922;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
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DE   Mdm2, transformed 3T3 cell double minute 2, p53 binding protein
DE   (Mouse).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA   Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA   Phelan M., Farmer A.;
RT   "Cloning of human full-length CDSs in BD Creator(TM) System Donor
RT   vector.";
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BT007258; AAP35922.1; -.
SQ   SEQUENCE   491 AA;  55232 MW;  F37CE163876BC983 CRC64;

  Query Match             99.3%;  Score 550;  DB 2;  Length 491;
  Best Local Similarity   99.1%;  Pred. No. 3.1e-50;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 6
AAH67077
ID   AAH67077    PRELIMINARY;      PRT;   491 AA.
AC   AAH67077;
DT   14-APR-2004 (TrEMBLrel. 27, Created)
DT   14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT   14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle;
RA   Strausberg R.;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC067077; AAH67077.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   491 AA;  55232 MW;  F37CE163876BC983 CRC64;

  Query Match             99.3%;  Score 550;  DB 2;  Length 491;
  Best Local Similarity   99.1%;  Pred. No. 3.1e-50;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 7
MDM2_CANFA
ID   MDM2_CANFA     STANDARD;      PRT;   487 AA.
AC   P56950; Q95KN5;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein
DE   Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Cdm2).
GN   Name=MDM2;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE OF 1-484 FROM N.A.
RX   MEDLINE=20218866; PubMed=10754200;
RA   Nasir L., Burr P.D., McFarlane S.T., Gault E., Thompson H.,
RA   Argyle D.J.;
RT   "Cloning, sequence analysis and expression of the cDNAs encoding the
RT   canine and equine homologues of the mouse double minute 2 (mdm2)
RT   proto-oncogene.";
RL   Cancer Lett. 152:9-13(2000).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS MDM2 AND MDM2-ALPHA).
RX   MEDLINE=20065171; PubMed=10597303;
RA   Veldhoen N., Metcalfe S., Milner J.;
RT   "A novel exon within the mdm2 gene modulates translation initiation in
RT   vitro and disrupts the p53-binding domain of mdm2 protein.";
RL   Oncogene 18:7026-7033(1999).
CC   -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC       apoptosis by binding its transcriptional activation domain.
CC       Functions as a ubiquitin ligase E3, in the presence of E1 and E2,
CC       toward p53 and itself. Permits the nuclear export of p53 and
CC       targets it for proteasome-mediated proteolysis (By similarity).
CC   -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity (By
CC       similarity).
CC   -!- SUBUNIT: Binds p53, p73, ARF(P14), ribosomal protein L5 and
CC       specifically to RNA. Can interact also with retinoblastoma protein
CC       (RB), E1A-associated protein EP300 and the E2F1 transcription
CC       factor (By similarity).
CC   -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed
CC       predominantly in the nucleoplasm (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Mdm2;
CC         IsoId=P56950-1; Sequence=Displayed;
CC       Name=Mdm2-alpha;
CC         IsoId=P56950-2; Sequence=VSP_003206;
CC   -!- TISSUE SPECIFICITY: Isoform Mdm2-alpha is present in lymphoid and
CC       testicular tissues.
CC   -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its
CC       G1 arrest and apoptosis functions. It also binds p73 and E2F1.
CC       Region II contains most of a central acidic region required for
CC       interaction with ribosomal protein L5 and a putative C4-type zinc
CC       finger. The RING finger domain which coordinates two molecules of
CC       zinc interacts specifically with RNA whether or not zinc is
CC       present and mediates the hetero-oligomerization with MDM4. It is
```

```
CC       also essential for its ubiquitin ligase E3 activity toward p53 and
CC       itself (By similarity).
CC   -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.
CC   -!- SIMILARITY: Contains 1 RanBP2-type zinc finger.
CC   -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC   -!- SIMILARITY: Contains 1 SWIB domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF100705; AAF67833.1; -.
DR   EMBL; AF322416; AAG42840.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Alternative splicing; Ligase; Metal-binding; Nuclear protein;
KW   Ubl conjugation pathway; Zinc; Zinc-finger.
FT   DOMAIN       27    107       SWIB.
FT   DOMAIN      179    185       Nuclear localization signal (Potential).
FT   DOMAIN      190    202       Nuclear export signal.
FT   DOMAIN      210    304       ARF-binding.
FT   DOMAIN      210    215       Poly-Ser.
FT   DOMAIN      242    331       Region II.
FT   DOMAIN      243    301       Asp/Glu-rich (acidic).
FT   ZN_FING     299    328       RanBP2-type.
FT   ZN_FING     434    475       RING-type.
FT   DOMAIN      462    469       Nucleolar localization signal
FT                                (Potential).
FT   VARSPLIC      1     61       Missing (in isoform Mdm2-alpha).
FT                                /FTId=VSP_003206.
FT   CONFLICT     11     11       G -> D (in Ref. 2).
FT   CONFLICT    238    239       QD -> HH (in Ref. 2).
SQ   SEQUENCE   487 AA;  54696 MW;  60CDB470A32A8E69 CRC64;

  Query Match             97.1%;  Score 538;  DB 1;  Length 487;
  Best Local Similarity   96.3%;  Pred. No. 5.9e-49;
  Matches  105;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||::||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVIFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||||||||||||||| | ||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQHEPSDSGTSVSEN 125


RESULT 8
Q9GMZ6
ID   Q9GMZ6      PRELIMINARY;      PRT;   487 AA.
AC   Q9GMZ6;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   MDM2.
GN   Name=mdm2;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Setoguchi A., Tsujimoto H.;
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB031276; BAB11975.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   GO; GO:0005730; C:nucleolus; ISS.
DR   GO; GO:0005654; C:nucleoplasm; ISS.
DR   GO; GO:0017163; F:negative regulator of basal transcription a. . .; ISS.
DR   GO; GO:0005515; F:protein binding; ISS.
DR   GO; GO:0000122; P:negative regulation of transcription from P. . .; ISS.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB_MDM2.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
SQ   SEQUENCE   487 AA;  54724 MW;  34FC5CC6A18D7744 CRC64;

  Query Match             97.1%;  Score 538;  DB 2;  Length 487;
  Best Local Similarity   96.3%;  Pred. No. 5.9e-49;
  Matches  105;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||::||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVIFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||||||||||||||| | ||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQHEPSDSGTSVSEN 125


RESULT 9
MDM2_HORSE
ID   MDM2_HORSE     STANDARD;      PRT;   491 AA.
AC   P56951;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein
DE   Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Edm2).
GN   Name=MDM2;
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20218866; PubMed=10754200;
RA   Nasir L., Burr P.D., McFarlane S.T., Gault E., Thompson H.,
RA   Argyle D.J.;
RT   "Cloning, sequence analysis and expression of the cDNAs encoding the
RT   canine and equine homologues of the mouse double minute 2 (mdm2)
RT   proto-oncogene.";
RL   Cancer Lett. 152:9-13(2000).
CC   -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC       apoptosis by binding its transcriptional activation domain.
CC       Functions as a ubiquitin ligase E3, in the presence of E1 and E2,
CC       toward p53 and itself. Permits the nuclear export of p53 and
CC       targets it for proteasome-mediated proteolysis (By similarity).
CC   -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity (By
CC       similarity).
CC   -!- SUBUNIT: Binds p53, p73, ARF(P14), ribosomal protein L5 and
CC       specifically to RNA. Can interact also with retinoblastoma protein
CC       (RB), E1A-associated protein EP300 and the E2F1 transcription
CC       factor (By similarity).
CC   -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed
```

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CC       predominantly in the nucleoplasm (By similarity).
CC   -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its
CC       G1 arrest and apoptosis functions. It also binds p73 and E2F1.
CC       Region II contains most of a central acidic region required for
CC       interaction with ribosomal protein L5 and a putative C4-type zinc
CC       finger. The RING finger domain which coordinates two molecules of
CC       zinc interacts specifically with RNA whether or not zinc is
CC       present and mediates the hetero-oligomerization with MDM4. It is
CC       also essential for its ubiquitin ligase E3 activity toward p53 and
CC       itself (By similarity).
CC   -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.
CC   -!- SIMILARITY: Contains 1 RanBP2-type zinc finger.
CC   -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC   -!- SIMILARITY: Contains 1 SWIB domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF121140; AAF28866.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Ligase; Metal-binding; Nuclear protein; Ubl conjugation pathway; Zinc;
KW   Zinc-finger.
FT   DOMAIN       27    107       SWIB.
FT   DOMAIN      179    185       Nuclear localization signal (Potential).
FT   DOMAIN      190    202       Nuclear export signal.
FT   DOMAIN      210    304       ARF-binding.
FT   DOMAIN      210    215       Poly-Ser.
FT   DOMAIN      242    331       Region II.
FT   DOMAIN      243    301       Asp/Glu-rich (acidic).
FT   ZN_FING     299    328       RanBP2-type.
FT   ZN_FING     438    479       RING-type.
FT   DOMAIN      466    473       Nucleolar localization signal
FT                                (Potential).
SQ   SEQUENCE   491 AA;  55279 MW;  641E033D5C1DEC39 CRC64;

  Query Match             97.1%;  Score 538;  DB 1;  Length 491;
  Best Local Similarity   96.3%;  Pred. No. 5.9e-49;
  Matches  105;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||::||||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVIFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||||||||||||:||| ||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVSQQEPSDSGTSVSEN 125


RESULT 10
Q7YRZ8
ID   Q7YRZ8      PRELIMINARY;      PRT;   491 AA.
AC   Q7YRZ8;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Double minute 2 protein MDM2.
GN   Name=mdm2;
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Miki R., Okuda M., Ma Z., Inokuma H., Onishi T.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB099709; BAC78209.1; -.
DR   GO; GO:0005730; C:nucleolus; ISS.
DR   GO; GO:0005654; C:nucleoplasm; ISS.
DR   GO; GO:0017163; F:negative regulator of basal transcription a. . .; ISS.
DR   GO; GO:0005515; F:protein binding; ISS.
DR   GO; GO:0000122; P:negative regulation of transcription from P. . .; ISS.
DR   InterPro; IPR003121; SWIB_MDM2.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
SQ   SEQUENCE   491 AA;  55433 MW;  D93E25D638E88934 CRC64;

  Query Match             96.6%;  Score 535;  DB 2;  Length 491;
  Best Local Similarity   95.4%;  Pred. No. 1.2e-48;
  Matches  104;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||:|||||||||||||||||||||||||||||||::||||||||||||||||||||||
Db         17 SQMPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVIFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||| | ||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQHEPSDSGTSVSEN 125


RESULT 11
Q8WYJ2
ID   Q8WYJ2      PRELIMINARY;      PRT;   436 AA.
AC   Q8WYJ2;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   MDM2 protein.
GN   Name=MDM2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21248713; PubMed=11351297;
RA   Tamborini E., Della Torre G., Lavarino C., Azzarelli A.,
RA   Carpinelli P., Pierotti M.A., Pilotti S.;
RT   "Analysis of the molecular species generated by MDM2 gene
RT   amplification in liposarcomas.";
RL   Int. J. Cancer 92:790-796(2001).
DR   EMBL; AF092844; AAL40179.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   GO; GO:0005730; C:nucleolus; ISS.
DR   GO; GO:0005654; C:nucleoplasm; ISS.
DR   GO; GO:0017163; F:negative regulator of basal transcription a. . .; ISS.
DR   GO; GO:0005515; F:protein binding; ISS.
DR   GO; GO:0000122; P:negative regulation of transcription from P. . .; ISS.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB_MDM2.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
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DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
SQ   SEQUENCE   436 AA;  49248 MW;  3C8F55E98BC4203A CRC64;

  Query Match           90.3%;  Score 500;  DB 2;  Length 436;
  Best Local Similarity   93.3%;  Pred. No. 6.1e-45;
  Matches   98;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTS 105
              |||||||||||||||||||||||||||||||||| :    |
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQEENSDELS 121


RESULT 12
MDM2_MOUSE
ID   MDM2_MOUSE     STANDARD;      PRT;   489 AA.
AC   P23804; Q61040; Q64330;
DT   01-NOV-1991 (Rel. 20, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein
DE   Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein).
GN   Name=Mdm2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM MDM2-P90).
RX   MEDLINE=91224107; PubMed=2026149;
RA   Fakharzadeh S.S., Trusko S.P., George D.L.;
RT   "Tumorigenic potential associated with enhanced expression of a gene
RT   that is amplified in a mouse tumor cell line.";
RL   EMBO J. 10:1565-1569(1991).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM MDM2-P90).
RC   STRAIN=129/Sv;
RX   MEDLINE=97074674; PubMed=8917101;
RA   Jones S.N., Ansari-Lari M.A., Hancock A.R., Jones W.J., Gibbs R.A.,
RA   Donehower L.A., Bradley A.;
RT   "Genomic organization of the mouse double minute 2 gene.";
RL   Gene 175:209-213(1996).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM MDM2-P90).
RC   STRAIN=129/Sv;
RX   MEDLINE=96299630; PubMed=8660994;
RA   de Oca Luna R.M., Tabor A.D., Eberspaecher H., Hulboy D.L.,
RA   Worth L.L., Colman M.S., Finlay C.A., Lozano G.;
RT   "The organization and expression of the mdm2 gene.";
RL   Genomics 33:352-357(1996).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORMS MDM2-P90 AND MDM2-P76).
RX   MEDLINE=99175199; PubMed=10075719;
RA   Saucedo L.J., Myers C.D., Perry M.E.;
RT   "Multiple murine double minute gene 2 (MDM2) proteins are induced by
RT   ultraviolet light.";
RL   J. Biol. Chem. 274:8161-8168(1999).
RN   [5]
RP   NUCLEOLAR LOCALIZATION SIGNAL.
RX   MEDLINE=20180080; PubMed=10713175;
RA   Weber J.D., Kuo M.-L., Bothner B., DiGiammarino E.L., Kriwacki R.W.,
RA   Roussel M.F., Sherr C.J.;
RT   "Cooperative signals governing ARF-mdm2 interaction and nucleolar
RT   localization of the complex.";
RL   Mol. Cell. Biol. 20:2517-2528(2000).
RN   [6]
RP   PHOSPHORYLATION BY ATM.
RX   MEDLINE=20079591; PubMed=10611322;
RA   Khosravi R., Maya R., Gottlieb T., Oren M., Shiloh Y., Shkedy D.;
RT   "Rapid ATM-dependent phosphorylation of MDM2 precedes p53 accumulation
RT   in response to DNA damage.";
RL   Proc. Natl. Acad. Sci. U.S.A. 96:14973-14977(1999).
CC   -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC       apoptosis by binding its transcriptional activation domain.
CC       Functions as a ubiquitin ligase E3, in the presence of E1 and E2,
CC       toward p53 and itself. Permits the nuclear export of p53 and
CC       targets it for proteasome-mediated proteolysis.
CC   -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity.
CC   -!- SUBUNIT: Binds p53, p73, ARF(P14), ribosomal protein L5 and
CC       specifically to RNA. Can interact also with retinoblastoma protein
CC       (RB), E1A-associated protein EP300 and the E2F1 transcription
CC       factor.
CC   -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed
CC       predominantly in the nucleoplasm. Interaction with ARF(P14)
CC       results in the localization of both proteins to the nucleolus. The
CC       nucleolar localization signals in both ARF(P14) and MDM2 may be
CC       necessary to allow efficient nucleolar localization of both
CC       proteins.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Mdm2-p90;
CC         IsoId=P23804-1; Sequence=Displayed;
CC         Note=Isoform Mdm2-p76 can also be produced by alternative
CC         initiation at Met-50 of isoform Mdm2-p90, but is produced more
CC         efficiently by alternative splicing;
CC       Name=Mdm2-p76;
CC         IsoId=P23804-2; Sequence=VSP_003215;
CC         Note=Does not bind to p53;
CC       Event=Alternative initiation;
CC         Comment=2 isoforms, Mdm2-p90 (shown here) and Mdm2-p76, are
CC         produced by alternative initiation at Met-1 and Met-50. Isoform
CC         Mdm2-p76 is produced more efficiently by alternative splicing;
CC   -!- TISSUE SPECIFICITY: Ubiquitously expressed at low-level throughout
CC       embryo development and in adult tissues. MDM2-p90 is much more
CC       abundant than MDM2-p76 in testis, brain, heart, and kidney, but in
CC       the thymus, spleen, and intestine, the levels of the MDM2 proteins
CC       are roughly equivalent.
CC   -!- INDUCTION: By UV light.
CC   -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its
CC       G1 arrest and apoptosis functions. It also binds p73 and E2F1.
CC       Region II contains most of a central acidic region required for
CC       interaction with ribosomal protein L5 and a putative C4-type zinc
CC       finger. The RING finger domain which coordinates two molecules of
CC       zinc interacts specifically with RNA whether or not zinc is
CC       present and mediates the hetero-oligomerization with MDM4. It is
CC       also essential for its ubiquitin ligase E3 activity toward p53 and
CC       itself.
CC   -!- PTM: Phosphorylated in response to ionizing radiation in an ATM-
CC       dependent manner.
CC   -!- DISEASE: The gene for this protein is amplified in a mouse tumor
CC       cell line.
CC   -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.
CC   -!- SIMILARITY: Contains 1 RanBP2-type zinc finger.
CC   -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC   -!- SIMILARITY: Contains 1 SWIB domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X58876; CAA41684.1; -.
DR   EMBL; U40145; AAA91167.1; -.
DR   EMBL; U47944; AAB09030.1; -.
DR   EMBL; U47935; AAB09030.1; JOINED.
DR   EMBL; U47936; AAB09030.1; JOINED.
DR   EMBL; U47937; AAB09030.1; JOINED.
DR   EMBL; U47938; AAB09030.1; JOINED.
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DR   EMBL; U47939; AAB09030.1; JOINED.
DR   EMBL; U47940; AAB09030.1; JOINED.
DR   EMBL; U47941; AAB09030.1; JOINED.
DR   EMBL; U47942; AAB09030.1; JOINED.
DR   EMBL; U47943; AAB09030.1; JOINED.
DR   EMBL; U47934; AAB09031.1; -.
DR   PIR; S15349; S15349.
DR   HSSP; Q9UMT8; 1YCR.
DR   MGD; MGI:96952; Mdm2.
DR   GO; GO:0005634; C:nucleus; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0004842; F:ubiquitin-protein ligase activity; IDA.
DR   GO; GO:0030163; P:protein catabolism; IDA.
DR   GO; GO:0016567; P:protein ubiquitination; IDA.
DR   GO; GO:0007089; P:traversing start control point of mitotic c. . .; IDA.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Alternative initiation; Alternative splicing; Ligase; Metal-binding;
KW   Nuclear protein; Phosphorylation; Proto-oncogene;
KW   Ubl conjugation pathway; Zinc; Zinc-finger.
FT   CHAIN         1    489       Ubiquitin-protein ligase E3 Mdm2, isoform
FT                                Mdm2-p90.
FT   CHAIN        50    489       ubiquitin-protein ligase E3 Mdm2, isoform
FT                                Mdm2-p76.
FT   INIT_MET      50     50       For isoform Mdm2-p76.
FT   DOMAIN        27    107       SWIB.
FT   DOMAIN       176    182       Nuclear localization signal (Potential).
FT   DOMAIN       183    195       Nuclear export signal.
FT   DOMAIN       203    213       Poly-Ser.
FT   DOMAIN       208    302       ARF-binding.
FT   DOMAIN       240    329       Region II.
FT   DOMAIN       221    299       Asp/Glu-rich (acidic).
FT   ZN_FING      297    326       RanBP2-type.
FT   ZN_FING      436    477       RING-type.
FT   DOMAIN       464    471       Nucleolar localization signal
FT                                (Potential).
FT   VARSPLIC       1     49       Missing (in isoform Mdm2-p76).
FT                                /FTId=VSP_003215.
FT   CONFLICT     203    203       S -> T (in Ref. 1).
FT   CONFLICT     419    419       D -> H (in Ref. 1).
FT   CONFLICT     486    486       S -> T (in Ref. 3).
SQ   SEQUENCE   489 AA;  54543 MW;  4ABF489E92038DF4 CRC64;

  Query Match             88.5%;  Score 490.5;  DB 1;  Length 489;
  Best Local Similarity   87.2%;  Pred. No. 7.3e-44;
  Matches   95;  Conservative    8;  Mismatches    3;  Indels    3;  Gaps    1;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              |||||||||||||||||||||||||||| ||||||:::|:|||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQNDTYTMKEIIFYIGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||:|||||||||||||| ||||||| |:||   |||||:||:
Db         77 CSNDLLGDVFGVPSPSVKEHRKIYAMIYRNLVAVSQQ---DSGTSLSES 122


RESULT 13
Q91XK7
ID   Q91XK7      PRELIMINARY;      PRT;   489 AA.
AC   Q91XK7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Mus musculus adult male lung cDNA, RIKEN full-length enriched library,
DE   clone:1200011P22 product:transformed mouse 3T3 cell double minute 2,
DE   full insert sequence (Transformed mouse 3T3 cell double minute 2) (Mus
DE   musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length
DE   enriched library, clone:E430022B10 product:transformed mouse 3T3 cell
DE   double minute 2, full insert sequence).
GN   Name=Mdm2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;
RX   MEDLINE=99279253; PubMed=10349636;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;
RX   MEDLINE=21085660; PubMed=11217851;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;
RX   MEDLINE=20499374; PubMed=11042159;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;
RX   MEDLINE=20530913; PubMed=11076861;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Lung;
RA   Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA   Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA   Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA   Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA   Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA   Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA   Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA   Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA   Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA   Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Mouse;
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RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [8]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Mouse;
RA   Strausberg R.;
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
RN   [9]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NOD; TISSUE=Thymus;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK004719; BAB23502.1; -.
DR   EMBL; BC050902; AAH50902.1; -.
DR   EMBL; AK088638; BAC40470.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   MGD; MGI:96952; Mdm2.
DR   GO; GO:0005730; C:nucleolus; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0004842; F:ubiquitin-protein ligase activity; IDA.
DR   GO; GO:0030163; P:protein catabolism; IDA.
DR   GO; GO:0016567; P:protein ubiquitination; IDA.
DR   GO; GO:0007089; P:traversing start control point of mitotic c. . .; IDA.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB_MDM2.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
SQ   SEQUENCE   489 AA;  54557 MW;  4ABF489A82038DF4 CRC64;

  Query Match             88.5%;  Score 490.5;  DB 2;  Length 489;
  Best Local Similarity   87.2%;  Pred. No. 7.3e-44;
  Matches   95;  Conservative    8;  Mismatches    3;  Indels    3;  Gaps    1;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||| |||||||:::|:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQNDTYTMKEIIFYIGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||:|||||||||||||| ||||||| |:||   |||||:||:
Db         77 CSNDLLGDVFGVPSFSVKEHRKIYAMIYRNLVAVSQQ---DSGTSLSES 122


RESULT 14
Q8WYJ3
ID   Q8WYJ3      PRELIMINARY;      PRT;   118 AA.
AC   Q8WYJ3;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   MDM2 protein (Fragment).
GN   Name=MDM2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21248713; PubMed=11351297;
RA   Tamborini E., Della Torre G., Lavarino C., Azzarelli A.,
RA   Carpinelli P., Pierotti M.A., Pilotti S.;
RT   "Analysis of the molecular species generated by MDM2 gene
RT   amplification in liposarcomas.";
RL   Int. J. Cancer 92:790-796(2001).
DR   EMBL; AF092843; AAL40178.1; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB_MDM2.
DR   Pfam; PF02201; SWIB; 1.
FT   NON_TER     118    118
SQ   SEQUENCE   118 AA;  13536 MW;  D7A4DBAA83D8841B CRC64;

  Query Match             85.4%;  Score 473;  DB 2;  Length 118;
  Best Local Similarity   98.9%;  Pred. No. 1.1e-42;
  Matches   92;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVV 93
              |||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVV 109


RESULT 15
MDM2_MESAU
ID   MDM2_MESAU     STANDARD;      PRT;   466 AA.
AC   Q60524;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein
DE   Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Fragment).
GN   Name=MDM2;
OS   Mesocricetus auratus (Golden hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC   Mesocricetus.
OX   NCBI_TaxID=10036;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pancreas;
RX   MEDLINE=95300112; PubMed=7780969;
RA   Chang K.W., Laconi S., Mangold K.A., Hubchak S., Scarpelli D.G.;
RT   "Multiple genetic alterations in hamster pancreatic ductal
RT   adenocarcinomas.";
RL   Cancer Res. 55:2560-2568(1995).
CC   -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC       apoptosis by binding its transcriptional activation domain.
CC       Functions as a ubiquitin ligase E3, in the presence of E1 and E2,
CC       toward p53 and itself. Permits the nuclear export of p53 and
```

```
CC       targets it for proteasome-mediated proteolysis (By similarity).
CC   -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity (By
CC       similarity).
CC   -!- SUBUNIT: Binds p53, p73, ARF(P14), ribosomal protein L5 and
CC       specifically to RNA. Can interact also with retinoblastoma protein
CC       (RB), E1A-associated protein EP300 and the E2F1 transcription
CC       factor (By similarity).
CC   -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed
CC       predominantly in the nucleoplasm (By similarity).
CC   -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its
CC       G1 arrest and apoptosis functions. It also binds p73 and E2F1.
CC       Region II contains most of a central acidic region required for
CC       interaction with ribosomal protein L5 and a putative C4-type zinc
CC       finger. The RING finger domain which coordinates two molecules of
CC       zinc interacts specifically with RNA whether or not zinc is
CC       present and mediates the hetero-oligomerization with MDM4. It is
CC       also essential for its ubiquitin ligase E3 activity toward p53 and
CC       itself (By similarity).
CC   -!- DISEASE: The gene for this protein is overexpressed in some
CC       tumors.
CC   -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.
CC   -!- SIMILARITY: Contains 1 RanBP2-type zinc finger.
CC   -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC   -!- SIMILARITY: Contains 1 SWIB domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U10982; AAC52425.1; -.
DR   HSSP; Q9UMT8; 1YCR.
DR   InterPro; IPR010984; MDM2.
DR   InterPro; IPR003121; SWIB.
DR   InterPro; IPR001876; Znf_RanGDP.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF02201; SWIB; 1.
DR   Pfam; PF00641; zf-RanBP; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01358; ZF_RANBP2_1; 1.
DR   PROSITE; PS50199; ZF_RANBP2_2; 1.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Ligase; Metal-binding; Nuclear protein; Proto-oncogene;
KW   Ubl conjugation pathway; Zinc; Zinc-finger.
FT   NON_TER       1      1
FT   DOMAIN       19     98       SWIB.
FT   DOMAIN      169    175       Nuclear localization signal (Potential).
FT   DOMAIN      176    188       Nuclear export signal.
FT   DOMAIN      196    201       Poly-Ser.
FT   DOMAIN      196    290       ARF-binding.
FT   DOMAIN      228    317       Region II.
FT   DOMAIN      209    287       Asp/Glu-rich (acidic).
FT   ZN_FING     285    314       RanBP2-type.
FT   ZN_FING     419    460       RING-type.
FT   DOMAIN      447    454       Nucleolar localization signal
FT                                (Potential).
FT   NON_TER     466    466
SQ   SEQUENCE   466 AA;  52390 MW;  78A3042163C5F939 CRC64;

  Query Match             84.6%;  Score 468.5;  DB 1;  Length 466;
  Best Local Similarity   86.2%;  Pred. No. 1.6e-41;
  Matches   94;  Conservative    7;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              |||||||||||||||| ||||||||||||||||::    ||||||||||||||||||
Db          9 SQIPASEQETLVRPKPLFLKLLKSVGAQKDTYTMKEII-LSWQYIMTKRLYDEKQQHIVY 67

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||:||||: |||||||||:|||:  |||||||:

Db         68 CSNDLLGDLFGVPSFSVKDHRKIHIMIYRNLVVVSQQETLQSGTSVSES 116

Search completed: January 27, 2005, 18:13:24
Job time : 85.6 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:45:30 ; Search time 80.8 Seconds
(without alignments)
483.929 Million cell updates/sec

Title: US-10-822-254-8
Perfect score: 554
Sequence: 1 SQIPASEQETLVRPKPLLLK.....NLVVVNQQESSDSGTSVSEN 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	550	99.3	284	2	AAR75494	Aar75494 Human dou
2	550	99.3	284	2	AAR75397	Aar75397 Human dou
3	550	99.3	491	2	AAR42175	Aar42175 Human MDM
4	550	99.3	491	2	AAR76696	Aar76696 Human MDM
5	550	99.3	491	2	AAW07887	Aaw07887 Human MDM
6	550	99.3	491	2	AAW15463	Aaw15463 Human MDM
7	550	99.3	491	2	AAW13380	Aaw13380 Human MDM
8	550	99.3	491	2	AAW13600	Aaw13600 Murine do
9	550	99.3	491	2	AAW48241	Aaw48241 Human MDM
10	550	99.3	491	2	AAW57241	Aaw57241 Human MDM
11	550	99.3	491	2	AAW42879	Aaw42879 Amino aci
12	550	99.3	491	2	AAW42971	Aaw42971 Amino aci
13	550	99.3	491	2	AAW94304	Aaw94304 Human MDM
14	550	99.3	491	3	AAY96567	Aay96567 MDM2 onco
15	550	99.3	491	4	AAB48284	Aab48284 Human MDM
16	550	99.3	491	5	AAE22654	Aae22654 Human Rin
17	550	99.3	491	5	AAE22698	Aae22698 Human Rin
18	550	99.3	491	5	AAE25913	Aae25913 Human dou
19	550	99.3	491	5	AAO15376	Aao15376 Human Dm2
20	550	99.3	491	7	ADD21815	Add21815 Human mdm
21	550	99.3	491	7	ADE61562	Ade61562 Human Pro
22	550	99.3	491	8	ADL23893	Adl23893 Human E3
23	550	99.3	491	8	ADO52353	Ado52353 Human p53
24	550	99.3	491	8	ADP12593	Adp12593 Protein e
25	550	99.3	491	8	ADN71936	Adn71936 MDM2 prot
26	550	99.3	491	8	ADQ19417	Adq19417 Human sof
27	550	99.3	1171	4	AAU32421	Aau32421 Novel hum
28	533.5	96.3	216	3	AAB08846	Aab08846 A human M
29	524.5	94.7	522	7	ADJ95152	Adj95152 Novel NOV
30	524.5	94.7	522	7	ADJ95154	Adj95154 Novel NOV
31	490.5	88.5	489	2	AAR42176	Aar42176 Murine MD
32	490.5	88.5	489	2	AAR76697	Aar76697 Mouse MDM
33	490.5	88.5	489	2	AAW07888	Aaw07888 Murine MD
34	490.5	88.5	489	2	AAW15464	Aaw15464 Murine MD
35	490.5	88.5	489	2	AAW48242	Aaw48242 Mouse MDM
36	490.5	88.5	489	2	AAW57246	Aaw57246 Mouse MDM
37	490.5	88.5	489	2	AAW42997	Aaw42997 Amino aci
38	490.5	88.5	489	2	AAW42972	Aaw42972 Amino aci
39	490.5	88.5	489	2	AAW94305	Aaw94305 Mouse MDM
40	490.5	88.5	489	5	AAE25914	Aae25914 Mouse dou
41	490.5	88.5	489	5	ABB57099	Abb57099 Mouse isc
42	490.5	88.5	489	5	AAO15375	Aao15375 Mouse Dm2
43	490.5	88.5	489	7	ADD21816	Add21816 Mouse mdm
44	490.5	88.5	489	7	ADE61560	Ade61560 Rat Prote
45	352	63.5	227	2	AAR75495	Aar75495 Human dou

ALIGNMENTS

RESULT 1
AAR75494
ID AAR75494 standard; protein; 284 AA.
XX
AC AAR75494;
XX
DT 02-FEB-1996 (first entry)
XX
DE Human double minute 2 (hdm-2) antibody-binding region fragment 1.
XX
KW Human double minute gene 2; hdm-2; antibody binding region; antigen;
KW cancer; sarcoma; rhabdomyosarcoma; diagnosis; immunoassay.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1. .284
FT /note= "amino acids 1-284 of hdm-2 gene product"
XX
PN DE4339533-A1.
XX
PD 14-JUN-1995.
XX
PF 19-NOV-1993; 93DE-04339533.
XX
PR 19-NOV-1993; 93DE-04339533.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Zentgraf H, Klein R, Frey M, Martens R;
XX
DR WPI; 1995-216248/29.
DR N-PSDB; AAQ92515.
XX
PT Detection of human double minute gene 2 (hdm-2) antibodies - by
PT incubation with new hdm-2 or antibody-binding hdm-2 fragments; useful in
PT the detection of specific cancers.
XX
PS Claim 11; Fig 1; 12pp; German.
XX
CC Fragments contg. amino acids 1-284, 58-284 and 58-491 of the hdm-2 (human
CC double minute 2) gene product are claimed. The overlapping protein
CC fragments contain binding regions for hdm-2- specific antibodies and are
CC useful for identifying such antibodies in a claimed immunoassay method.
CC The presence of anti-hdm-2 antibodies is diagnostic of certain forms of
CC cancer, e.g. rhabdomyosarcoma
XX
SQ Sequence 284 AA;

```
  Query Match             99.3%;  Score 550;  DB 2;  Length 284;
  Best Local Similarity   99.1%;  Pred. No. 3.6e-62;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 2
AAR75397
ID   AAR75397 standard; protein; 284 AA.
XX
AC   AAR75397;
XX
DT   25-MAR-2003  (revised)
DT   25-JAN-1996  (first entry)
XX
DE   Human double minute 2 (hdm-2) antibody-binding region fragment 1.
XX
KW   Human double minute gene 2; hdm-2; antibody binding region; antigen;
KW   cancer; sarcoma; rhabdomyosarcoma; diagnosis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .284
FT                   /note= "amino acids 1-284 of hdm-2 gene product"
XX
PN   DE4345249-A1.
XX
PD   24-MAY-1995.
XX
PF   19-NOV-1993;   93DE-04345249.
XX
PR   19-NOV-1993;   93DE-04339533.
XX
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI   Zentgraf H,  Klein R,  Frey M,  Martens R;
XX
DR   WPI; 1995-195167/26.
DR   N-PSDB; AAQ87261.
XX
PT   New hdm-2 fragments contg. antibody binding region - used to detect
PT   specific antibodies for diagnosis of cancers, also new DNA sequences
PT   encoding them.
XX
PS   Claim 2; Fig 1; 11pp; German.
XX
CC   Fragments contg. amino acids 1-284, 58-284 and 58-491 of the hdm-2 (human
CC   double minute 2) gene product are claimed. The overlapping protein
CC   fragments contain binding regions for hdm-2- specific antibodies and are
CC   useful for identifying such antibodies. The presence of anti-hdm-2
CC   antibodies is diagnostic of certain forms of cancer, e.g.
CC   rhabdomyosarcoma. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 284 AA;

  Query Match             99.3%;  Score 550;  DB 2;  Length 284;
  Best Local Similarity   99.1%;  Pred. No. 3.6e-62;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 3
AAR42175
ID   AAR42175 standard; protein; 491 AA.
XX
AC   AAR42175;
XX
DT   25-MAR-2003  (revised)
DT   05-MAY-1994  (first entry)
XX
DE   Human MDM2.
XX
KW   p53 gene; tumour suppressor gene; regulation; cellular proliferation;
KW   cellular transformation; carcinoma; human; tumour; MDM2; inhibition;
KW   gene amplification.
XX
OS   Homo sapiens.
XX
PN   WO9320238-A2.
XX
PD   14-OCT-1993.
XX
PF   07-APR-1993;   93WO-US003199.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Burrell M,  Hill DE,  Kinzler KW,  Vogelstein B;
XX
DR   WPI; 1993-336944/42.
DR   N-PSDB; AAQ49891.
XX
PT   Diagnosing neoplasia from amplification of MDM2 gene - or elevated gene
PT   expression, also new DNA, MDM2 protein, antibodies and treatment of
PT   sarcoma by inhibiting MDM2 expression.
XX
PS   Claim 19; Fig 1; 75pp; English.
XX
CC   This sequence is encoded by the MDM2 gene. Amplification of the MDM2 gene
CC   is diagnostic of neoplasia or the potential for neoplasia. The protein
CC   encoded by this gene interacts with the product of the p53 gene. p53 is a
CC   tumour-suppressor gene and encodes a protein which appears to be a member
CC   of a group of proteins which regulate normal cellular proliferation and
CC   suppression of cellular transformation. Inactivation of the p53 gene has
CC   been implicated in the formation, or progression of a wide variety of
CC   carcinoma. Polypeptides containing at least amino acids 13-41 of p53, or
CC   the DNA encoding these, may be used to inhibit the growth of tumour cells
CC   containing MDM2 gene amplification. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 491 AA;

  Query Match             99.3%;  Score 550;  DB 2;  Length 491;
  Best Local Similarity   99.1%;  Pred. No. 7.6e-62;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 4
AAR76696
ID   AAR76696 standard; protein; 491 AA.
```

```
XX
AC   AAR76696;
XX
DT   16-OCT-2003  (revised)
DT   01-NOV-1995  (first entry)
XX
DE   Human MDM2 protein.
XX
KW   MDM2; sarcoma; diagnostic; DNA probe.
XX
OS   Homo sapiens; (cell line CaCo-2).
XX
PN   US5420263-A.
XX
PD   30-MAY-1995.
XX
PF   07-APR-1993;   93US-00044619.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Vogelstein B,  Kinzler KW;
XX
DR   WPI; 1995-206312/27.
DR   N-PSDB; AAQ94589.
XX
PT   New human MDM2 cDNA - used to develop prods. for use in the diagnosis and
PT   treatment of tumours.
XX
PS   Claim 1; Col 23-26; 34pp; English.
XX
CC   The human MDM2 gene is genetically altered (i.e. amplified) in human
CC   tumour cells. The human MDM2 protein binds to human p53 and allows the
CC   cell to escape from p53-regulated growth. Detecting that the gene has
CC   become amplified or detecting increased gene product expression (using
CC   probes, proteins, antibodies and inhibitors) allows diagnosis and therapy
CC   of cancers such as colorectal carcinoma, lung cancer and chronic
CC   myelogenous leukaemia. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ   Sequence 491 AA;

  Query Match             99.3%;  Score 550;  DB 2;  Length 491;
  Best Local Similarity   99.1%;  Pred. No. 7.6e-62;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 5
AAW07887
ID   AAW07887 standard; protein; 491 AA.
XX
AC   AAW07887;
XX
DT   25-MAR-2003  (revised)
DT   28-JAN-1997  (first entry)
XX
DE   Human MDM-2, involved in tumour-development.
XX
KW   p53; MDM-2; binding-inhibitor; identification; tumour; cancer; neoplasia;
KW   antibody fusion protein; therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   166. .169
FT                   /label= phosphorylation_site
FT                   /note= "potential casein kinase II phosphorylation site"
FT   Binding-site    181. .185
FT                   /label= nuclear_localisation_signal
FT   Modified-site   192. .195
FT                   /label= phosphorylation_site
FT                   /note= "potential casein kinase II phosphorylation site"
FT   Domain          223. .274
FT                   /label= acid_activation_domain
FT   Modified-site   269. .272
FT                   /label= phosphorylation_site
FT                   /note= "potential casein kinase II phosphorylation site"
FT   Modified-site   290. .293
FT                   /label= phosphorylation_site
FT                   /note= "potential casein kinase II phosphorylation site"
FT   Domain          305. .322
FT                   /label= metal_binding_site
FT   Domain          461. .478
FT                   /label= metal_binding_site
XX
PN   US5550023-A.
XX
PD   27-AUG-1996.
XX
PF   18-MAY-1994;   94US-00245500.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
PR   07-APR-1993;   93US-00044619.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Vogelstein B,  Kinzler KW;
XX
DR   WPI; 1996-401591/40.
DR   N-PSDB; AAT45151.
XX
PT   Identification of cpds. interfering with human MDM2/p53 binding - useful
PT   as therapeutic agents to treat human neoplastic cells.
XX
PS   Claim 26; Col 25-28; 36pp; English.
XX
CC   AAW07887 represents human MDM-2 derived from a human colon carcinoma cell
CC   line, CaCo-2, cDNA library. The MDM-2 protein is used in a method for
CC   identifying compounds that interfere with the binding of p53 and MDM-2.
CC   In binding the p53 protein, the MDM-2 protein releases a cell from p53-
CC   regulated growth, allowing cancers to develop. Therefore compounds
CC   identified as interfering with the binding of MDM-2 to p53 are
CC   potentially useful in the treatment of human neoplastic cells. In the
CC   method pref. one or both of the proteins is a fusion protein esp. with an
CC   antibody or antibody fragment which aids separation and identification.
CC   (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 491 AA;

  Query Match             99.3%;  Score 550;  DB 2;  Length 491;
  Best Local Similarity   99.1%;  Pred. No. 7.6e-62;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 6
AAW15463
ID   AAW15463 standard; protein; 491 AA.
XX
```

```
AC   AAW15463;
XX
DT   25-MAR-2003  (revised)
DT   18-JUN-1997  (first entry)
XX
DE   Human MDM2.
XX
KW   Human; MDM2 protein; antibody; detection; cancer; diagnosis;
KW   p53-regulated growth.
XX
OS   Homo sapiens.
XX
PN   US5618921-A.
XX
PD   08-APR-1997.
XX
PF   17-FEB-1995;   95US-00390479.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
PR   07-APR-1993;   93US-00044619.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Vogelstein B,  Kinzler KW,  Burrell M,  Hill DE;
XX
DR   WPI; 1997-225474/20.
DR   N-PSDB; AAT66410.
XX
PT   Antibodies specific for human MDM2 protein - for diagnosis of cancer.
XX
PS   Claim 1; Col 19-24; 35pp; English.
XX
CC   This sequence represents the human MDM2 protein. Antibodies that
CC   specifically bind to human MDM2 protein may be used for detecting
CC   elevated expression of the MDM2 gene in a human tissue or body fluid
CC   sample, esp. for cancer diagnosis. The antibodies may be used to
CC   interfere with the binding of p53 to MDM2. Elevated levels of MDM2 appear
CC   to sequester p53 and allow the cell to escape from p53-regulated growth.
CC   (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 491 AA;

  Query Match             99.3%;  Score 550;  DB 2;  Length 491;
  Best Local Similarity   99.1%;  Pred. No. 7.6e-62;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 7
AAW13380
ID   AAW13380 standard; protein; 491 AA.
XX
AC   AAW13380;
XX
DT   25-MAR-2003  (revised)
DT   05-JUN-1997  (first entry)
XX
DE   Human MDM2 protein.
XX
KW   Human; MDM2; CaCo-2; colonic; carcinoma; probe; detection; amplification;
KW   elevation; expression; diagnosis; neoplasia; neoplastic transformation;
KW   sarcoma; colorectal; lung cancer; chronic myelogenous leukaemia.
XX
OS   Homo sapiens.
XX
PN   US5606044-A.
XX
PD   25-FEB-1997.
XX
PF   17-FEB-1995;   95US-00390546.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
PR   07-APR-1993;   93US-00044619.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Kinzler KW,  Vogelstein B,  Hill DE,  Burrell M;
XX
DR   WPI; 1997-153623/14.
DR   N-PSDB; AAT62065.
XX
PT   Detection of amplification of human MDM2 gene - useful for diagnosis of
PT   neoplasia or potential neoplastic transformation.
XX
PS   Example 1; Col 21-24; 35pp; English.
XX
CC   The present sequence is the human MDM2 protein, the cDNA for which was
CC   isolated from a human CaCo-2 colonic carcinoma cell cDNA library using a
CC   murine MDM2 cDNA probe. The MDM2 cDNA can be used as a probe to detect
CC   the amplification or elevated expression of a human MDM2 gene, which is
CC   diagnostic of neoplasia or the potential for neoplastic transformation,
CC   useful for the detection of, e.g. sarcomas, colorectal carcinoma, lung
CC   cancer and chronic myelogenous leukaemia. (Updated on 25-MAR-2003 to
CC   correct PF field.)
XX
SQ   Sequence 491 AA;

  Query Match             99.3%;  Score 550;  DB 2;  Length 491;
  Best Local Similarity   99.1%;  Pred. No. 7.6e-62;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 8
AAW13600
ID   AAW13600 standard; protein; 491 AA.
XX
AC   AAW13600;
XX
DT   16-JAN-1998  (first entry)
XX
DE   Murine double minute 2 protein sequence.
XX
KW   Mouse; Mdm2; murine double minute; phosphoprotein; binding; modulation;
KW   tumour suppressor; p53; oncogene; cell cycle arrest; p107; antagonist;
KW   inhibition; transcription factor; adenocarcinoma; colon; cancer; breast;
KW   lung; stomach; myeloid leukaemia; lymphoma; hyperproliferative;
KW   restenosis.
XX
OS   Mus musculus.
XX
PN   WO9709343-A2.
XX
PD   13-MAR-1997.
XX
PF   02-SEP-1996;   96WO-FR001340.
XX
PR   04-SEP-1995;   95FR-00010331.
XX
PA   (RHON ) RHONE POULENC RORER SA.
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PA (INRM) INST NAT SANTE & RECH MEDICALE.
XX
PI Tocque B, Dubs-Poterszman M, Wasylyk B;
XX
DR WPI; 1997-192837/17.
DR N-PSDB; AAT61637.
XX
PT Treating cancer with antagonist of oncogenic activity of protein Mdm2 -
PT or nucleic acid encoding an antagonist, also viral vectors contg. this
PT nucleic acid.
XX
PS Claim 2; Page 26-30; 43pp; French.
XX
CC This is the amino acid sequence of the mouse Mdm2 (murine double minute-
CC 2) protein, a 90 kD phosphoprotein which binds and modulates the activity
CC of the tumour suppressor protein p53. It has now been shown that the mdm2
CC protein itself has oncogenic properties, especially in a p53-null
CC background. Mdm2 is observed to unblock cell cycle arrest in G1 caused by
CC over-expression of the p107 protein. This is especially done by the
CC region covering amino acid 1-134. The invention therefore relates to
CC antagonists able to inhibit the oncogenic activity of mdm2. These include
CC fragments of the p53 protein, especially amino acids 1-52, 1-41, 6-41, 16
CC -25 or 18-23 (AAW13602-6), or fragments of transcription factors e.g.
CC TFII, TBP or TAF250, which bind amino acids 1-134 of mdm2. Other
CC inhibitors include compounds which disrupt binding to region 135-491 of
CC mdm2, e.g. Rb, L5 or the transcription factor E2F. The antagonists are
CC used to treat e.g. adenocarcinoma of the colon; cancer of the breast,
CC lung or stomach; myeloid leukaemia; B cell lymphoma, or other
CC hyperproliferative conditions such as restenosis
XX
SQ Sequence 491 AA;

Query Match 99.3%; Score 550; DB 2; Length 491;
Best Local Similarity 99.1%; Pred. No. 7.6e-62;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
|||||||||||||||||||||||||||||||||||||||||||||||||||
Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125

RESULT 9
AAW48241
ID AAW48241 standard; protein; 491 AA.
XX
AC AAW48241;
XX
DT 18-JUN-1998 (first entry)
XX
DE Human MDM2.
XX
KW Human; MDM2; hMDM2; tumour; cancer; diagnosis; neoplastic disease;
KW sarcoma; liposarcoma; malignant fibrous histiocytoma; osteosarcoma.
XX
OS Homo sapiens.
XX
PN US5736338-A.
XX
PD 07-APR-1998.
XX
PF 17-FEB-1995; 95US-00390517.
XX
PR 07-APR-1992; 92US-00867840.
PR 23-JUN-1992; 92US-00903103.
PR 07-APR-1993; 93US-00044619.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Vogelstein B, Kinzler KW, Hill DE, Burrell M;
XX
DR WPI; 1998-239206/21.
DR N-PSDB; AAV20549.
XX
PT Cancer diagnosis - by determination of MDM2 protein.
XX
PS Claim 1; Col 25-28; 35pp; English.
XX
CC The present sequence represents human MDM2 (hMDM2) which is used in the
CC method of the present invention. The present invention describes a method
CC for diagnosing a neoplastic disease caused by overexpression of MDM2
CC protein. The method comprises detecting an elevated cellular amount of
CC this protein. The method is useful for the diagnosis of sarcoma,
CC especially liposarcoma, malignant fibrous histiocytoma or osteosarcoma
XX
SQ Sequence 491 AA;

Query Match 99.3%; Score 550; DB 2; Length 491;
Best Local Similarity 99.1%; Pred. No. 7.6e-62;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
|||||||||||||||||||||||||||||||||||||||||||||||||||
Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125

RESULT 10
AAW57241
ID AAW57241 standard; protein; 491 AA.
XX
AC AAW57241;
XX
DT 10-AUG-1998 (first entry)
XX
DE Human MDM2 protein.
XX
KW Human; p53; MDM2; tumour; growth inhibition; amplification;
KW malignant fibrous histiocytoma; liposarcoma.
XX
OS Homo sapiens.
XX
PN US5756455-A.
XX
PD 26-MAY-1998.
XX
PF 17-FEB-1995; 95US-00390515.
XX
PR 07-APR-1992; 92US-00867840.
PR 23-JUN-1992; 92US-00903103.
PR 07-APR-1993; 93US-00044619.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Vogelstein B, Kinzler KW;
XX
DR WPI; 1998-321574/28.
DR N-PSDB; AAV28876.
XX
PT Inhibiting growth of tumour cells having MDM2 gene amplification - with
PT p53 protein fragment.
XX
PS Claim 1; Col 23-28; 40pp; English.
XX
CC A method has been developed for inhibiting the growth of tumour cells
CC containing a human MDM2 gene amplification. The method comprises treating
CC the tumour cells with a DNA molecule that expresses a polypeptide capable
CC of binding to human MDM2 protein. The present sequence represents human
CC MDM2 protein. The present invention describes three preferred
CC polypeptides for binding human MDM2: (1) the polypeptide comprises amino

```
CC   acids 1-50 of p53 (see AAW57240); (2) the polypeptide comprises amino
CC   acids 13-41 of p53 (see AAW57240) and at least none additional p53
CC   residues on the N- or C-terminal side, provided that the polypeptide
CC   lacks the homooligomerisation domain of p53; (3) the polypeptide
CC   comprises amino acids 13-41 of p53 (see AAW57241) and at least nine
CC   additional p53 residues on the N- or C-terminal side, provided that the
CC   polypeptide lacks amino acids 138-393 of p53. Some malignant fibrous
CC   histiocytomas and liposarcomas have an MDM2 gene amplification, so
CC   detection of increased expression of MDM2 gene products indicates
CC   tumourigenesis
XX
SQ   Sequence 491 AA;

  Query Match             99.3%;  Score 550;  DB 2;  Length 491;
  Best Local Similarity   99.1%;  Pred. No. 7.6e-62;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 11
AAW42879
ID   AAW42879 standard; protein; 491 AA.
XX
AC   AAW42879;
XX
DT   30-APR-1998  (first entry)
XX
DE   Amino acid sequence of human MDM2.
XX
KW   MDM2; tumour; diagnosis; neoplasia; DNA binding protein; p53 polypeptide;
KW   binding; tumour cell; p53-regulated growth; inhibition;
KW   anti-cancer agent.
XX
OS   Homo sapiens.
XX
PN   US5708136-A.
XX
PD   13-JAN-1998.
XX
PF   17-FEB-1995;   95US-00390516.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
PR   07-APR-1993;   93US-00044619.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Vogelstein B,  Kinzler KW,  Burrell M,  Hill DE;
XX
DR   WPI; 1998-100408/09.
XX
PT   Human MDM2 binding polypeptide - comprises fragments of p53, useful in re
PT   -establishing p53-regulated growth control in cells over-expressing MDM2.
XX
PS   Disclosure; Col 23-28; 41pp; English.
XX
CC   The present sequence represents human MDM2. The MDM2 gene is amplified in
CC   some human tumours. The amplification of this gene is diagnostic of
CC   neoplasia or its potential. It is speculated that the MDM2 protein is a
CC   potential DNA binding protein that functions in the modulation of
CC   expression of other genes and, when present in excess, inteferes with
CC   normal constraints on cell growth. A cell containing three recombinant
CC   DNA constructs was produced. These constructs encode an MDM2 protein
CC   fused to a sequence-specific DNA binding domain, a p53 polypeptide fused
CC   to a transcriptional activation domain, and a reporter gene downstream
CC   from a DNA element which is recognised by the sequence-specific DNA-
CC   binding domain. The cell is used to identify a compound which interferes
CC   with the binding of MDM2 and p53. Since MDM2 is overexpressed in tumour
CC   cells and since binding of MDM2 to p53 appears to allow tumour cells to
CC   escape from p53-regulated growth, compounds that inhibit such binding
CC   would be useful as anti-cancer agents
XX
SQ   Sequence 491 AA;

  Query Match             99.3%;  Score 550;  DB 2;  Length 491;
  Best Local Similarity   99.1%;  Pred. No. 7.6e-62;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 12
AAW42971
ID   AAW42971 standard; protein; 491 AA.
XX
AC   AAW42971;
XX
DT   29-APR-1998  (first entry)
XX
DE   Amino acid sequence of human MDM2.
XX
KW   MDM2; tumour; diagnosis; neoplasia; DNA binding protein; p53 polypeptide;
KW   binding; tumour cell; p53-regulated growth; inhibition;
KW   anti-cancer agent.
XX
OS   Homo sapiens.
XX
PN   US5702903-A.
XX
PD   30-DEC-1997.
XX
PF   13-NOV-1995;   95US-00557393.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
PR   07-APR-1993;   93US-00044619.
PR   18-MAY-1994;   94US-00245500.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Vogelstein B,  Kinzler KW;
XX
DR   WPI; 1998-076411/07.
DR   N-PSDB; AAV03607.
XX
PT   Cell containing reporter construct containing human MDM2 and p53 genes -
PT   for identifying compounds that interfere with binding of human MDM2 to
PT   human p53, useful as anti-cancer agents.
XX
PS   Disclosure; Coulmns 22-28; 37pp; English.
XX
CC   The present sequence represents human MDM2. The MDM2 gene is amplified in
CC   some human tumours. The amplification of this gene is diagnostic of
CC   neoplasia or its potential. It is speculated that the MDM2 protein is a
CC   potential DNA binding protein that functions in the modulation of
CC   expression of other genes and, when present in excess, inteferes with
CC   normal constraints on cell growth. A cell containing three recombinant
CC   DNA constructs was produced. These constructs encode an MDM2 protein
CC   fused to a sequence-specific DNA binding domain, a p53 polypeptide fused
CC   to a transcriptional activation domain, and a reporter gene downstream
CC   from a DNA element which is recognised by the sequence-specific DNA-
CC   binding domain. The cell is used to identify a compound which interferes
CC   with the binding of MDM2 and p53. Since MDM2 is overexpressed in tumour
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CC   cells and since binding of MDM2 to p53 appears to allow tumour cells to
CC   escape from p53-regulated growth, compounds that inhibit such binding
CC   would be useful as anti-cancer agents
XX
SQ   Sequence 491 AA;

  Query Match             99.3%;  Score 550;  DB 2;  Length 491;
  Best Local Similarity   99.1%;  Pred. No. 7.6e-62;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 13
AAW94304
ID   AAW94304 standard; protein; 491 AA.
XX
AC   AAW94304;
XX
DT   13-APR-1999  (first entry)
XX
DE   Human MDM2.
XX
KW   Human; MDM2; p53; tumourigenesis; growth regulation; diagnosis;
KW   malignant fibrous histocytoma; MFH; liposarcoma.
XX
OS   Homo sapiens.
XX
PN   US5858976-A.
XX
PD   12-JAN-1999.
XX
PF   14-FEB-1997;   97US-00801718.
XX
PR   07-APR-1992;   92US-00867840.
PR   23-JUN-1992;   92US-00903103.
PR   07-APR-1993;   93US-00044619.
PR   17-FEB-1995;   95US-00390515.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Kinzler KW,  Vogelstein B;
XX
DR   WPI; 1999-152105/13.
DR   N-PSDB; AAX03947.
XX
PT   Inhibiting growth of tumour cells having MDM2 gene amplification - with
PT   MDM2-binding p53 fragment.
XX
PS   Claim 1; Col 23-28; 41pp; English.
XX
CC   The present invention describes: (1) a method for inhibiting the growth
CC   of tumour cells which contain a human MDM2 gene amplification, comprising
CC   administering to the cells a DNA molecule that expresses a polypeptide
CC   consisting of a portion of p53 i.e. amino acids 13-41 of the 64 amino
CC   acid sequence given in AAW94303, the polypeptide being capable of binding
CC   to human MDM2 (the present sequence); (2) a method as in (1) where the
CC   polypeptide lacks the homo-oligomerisation domain of p53; and (3) a
CC   method as in (1) where the polypeptide lacks amino acids 138-393 of p53.
CC   The method is useful for treating the following tumour types which have a
CC   MDM2 gene amplification: M-7 malignant fibrous histocytoma (MFH), M-20
CC   MFH, L-9 liposarcoma, KL7 liposarcoma, KL28 liposarcoma, KL30
CC   liposarcoma, and OSA-CL MFH
XX
SQ   Sequence 491 AA;

  Query Match             99.3%;  Score 550;  DB 2;  Length 491;
  Best Local Similarity   99.1%;  Pred. No. 7.6e-62;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 14
AAY96567
ID   AAY96567 standard; protein; 491 AA.
XX
AC   AAY96567;
XX
DT   12-SEP-2000  (first entry)
XX
DE   MDM2 oncoprotein.
XX
KW   hEST2; telomerase; catalytic subunit; reverse transcriptase; life-span;
KW   retinoblastoma; p53; tumour suppressor; inhibitor; arteriosclerosis;
KW   proliferation; immortal; tumour therapy; macular degeneration; activator;
KW   INK4; MDM2; oncoprotein.
XX
OS   Homo sapiens.
XX
PN   WO200031238-A2.
XX
PD   02-JUN-2000.
XX
PF   24-NOV-1999;   99WO-US027907.
XX
PR   25-NOV-1998;   98US-0109891P.
PR   17-FEB-1999;   99US-0120549P.
XX
PA   (GENE-) GENETICA INC.
XX
PI   Hannon GJ,  Beach DH;
XX
DR   WPI; 2000-400055/34.
DR   N-PSDB; AAA29389.
XX
PT   New method for increasing the proliferative capacity of cell lines
PT   comprises administering agents reversibly activating telomerase activity
PT   and reversibly inactivating Rb/INk4 and/or p53 pathways useful in
PT   treating age related diseases.
XX
PS   Claim 5; Page 120; 123pp; English.
XX
CC   The invention concerns methods and reagents for extending the life-span,
CC   e.g. the number of mitotic divisions, of a cell. The method relies on
CC   activation of a telomerase activity and inhibition of one or both of a
CC   retinoblastoma (Rb)/INK4 pathway or a p53 pathway. Phosphorylation of Rb
CC   by cyclin-dependent kinases, cdk4 and cdk6, releases the cells into the
CC   division cycle. Binding of INK4 family members, e.g. the tumour
CC   suppressor p16INK4a, inhibits kinase activity and results in growth
CC   arrest. Rb inactivators can selectively and reversibly inactivate an
CC   Rb/INK4 pathway, especially an Rb/p16INK4a pathway. The oncoprotein MDM2
CC   is a cellular inhibitor of Rb/E2F function and the p53 tumour suppressor
CC   and can also be used in the methods. Other molecules which can be used
CC   include cdk4 or cdk6 mutants. In particular, a cdk4 mutant is one which
CC   differs from at one or more of residues K22, R24, H95 and/or D97.
CC   Additional constructs include a papilloma virus E7 protein, or other
CC   viral oncoprotein which bypasses Rb and/or p53. Antisense constructs of
CC   the Rb and p16INK4a genes may also be used. The methods are useful for
CC   increasing the proliferative capacity of cells. The cells are
CC   subsequently of use in pharmaceutical and cosmetic preparations used to
CC   treat conditions related to (premature) ageing, e.g. macular degeneration
CC   and arteriosclerosis. The cells can also be used to replace tumour cell
CC   lines in vitro and for studies on biochemical and physiological aspects
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CC   of growth and differentiation. Long lived (immortal) cells could also be
CC   of use in the production of normal or genetically engineered
CC   biotechnology products
XX
SQ   Sequence 491 AA;

  Query Match             99.3%;  Score 550;  DB 3;  Length 491;
  Best Local Similarity   99.1%;  Pred. No. 7.6e-62;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


RESULT 15
AAB48284
ID   AAB48284 standard; protein; 491 AA.
XX
AC   AAB48284;
XX
DT   02-APR-2001  (first entry)
XX
DE   Human MDM2 protein.
XX
KW   S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF;
KW   CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;
KW   Bad; Bcl-2; tumour; cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO200075184-A1.
XX
PD   14-DEC-2000.
XX
PF   05-JUN-2000; 2000WO-US015449.
XX
PR   04-JUN-1999;   99US-0137494P.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Zhang H,  Tsvetkov LM,  Kondo T;
XX
DR   WPI; 2001-061703/07.
DR   N-PSDB; AAC84596.
XX
PT   Modulating polypeptide levels in a cell, diagnosing and treating tumor,
PT   involves altering levels of proteins such as S-phase kinase associated
PT   proteins 1, 2 and cullin/CDC53 proteins.
XX
PS   Claim 5; Page 93-95; 162pp; English.
XX
CC   The invention relates to methods of altering the polypeptide levels in a
CC   cell, using proteins selected from S-phase kinase associated proteins 1
CC   and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the
CC   cullin/ CDC53 family of proteins). The method is useful for altering the
CC   level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2
CC   polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for
CC   detecting tumours, and in monitoring tumor treatment in a mammal. Agents
CC   that modulate interactions between SKP and target proteins are useful for
CC   treating tumours
XX
SQ   Sequence 491 AA;

  Query Match             99.3%;  Score 550;  DB 4;  Length 491;
  Best Local Similarity   99.1%;  Pred. No. 7.6e-62;
  Matches  108;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLYYLGQYIMTKRLYDEKQQHIVY 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVY 76

Qy         61 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 109
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 CSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVVNQQESSDSGTSVSEN 125


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